

# JOURNAL OF CREATION

The background of the cover is a grayscale image of a snowball Earth, showing a globe covered in ice and landmasses. The globe is set against a dark blue space background with stars and nebulae. The text is overlaid on this image.

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**JUMPING BEETLE  
INSPIRES BIONIC DESIGN**

**BIBLICAL VIEW OF  
QUANTUM MECHANICS**

## **‘SNOWBALL EARTH’ GLACIATIONS: UNIFORMITARIAN CONUNDRUMS**

**ISAAC NEWTON—  
FOE OF CREATION?**

**AMAZINGLY COMPLEX  
TRANSFER RNA**





# JOURNAL OF CREATION

An international journal devoted to the presentation and discussion of technical aspects of the sciences such as geology, biology, astronomy, etc., and also geography, archaeology, biblical history, philosophy, etc., as they relate to the study of biblical creation and Noah's Flood.

**COVER:** Artistic impression of a frozen Earth

**IMAGE:** Rasslava © 123RF.com

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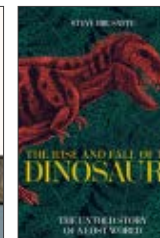
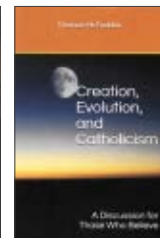
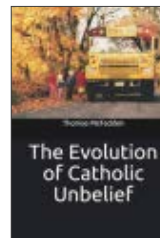
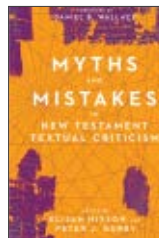
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# Newly discovered jumping beetle mechanism inspires bionic design

Gavin Cox

A new catapult mechanism has recently been discovered in the hind legs of certain beetles, astounding researchers with its ability to pack a powerful punch. These ‘flea beetles’ have been observed to display incredible jumping abilities, surpassing that of fleas. A recent paper, published by the online peer-reviewed scientific journal *ZooKeys*, describes their ability:

“The jumping of flea beetles is an extremely effective method to avoid potential predators, as it allows beetles [to] quickly disappear from the leaf surface, where they spend most of their life. *Blepharida sacra* can jump up to 70 cm or 100 times more than its body length, while *Longitarsus anchusae* reaches a jump of 289 times its body length; the average acceleration of *Psylliodes affinis* during take-off can be up to 266 times the acceleration of gravity [g].”<sup>1</sup>

Scaled up to human size, that would be like a 6 ft (1.8 m) tall long-jump athlete leaping more than half a kilometre! When we consider that fighter pilots can sustain no more than 9g for a few seconds, it is remarkable how these beetles survive nearly 30 times that force. Furthermore, these bouncing bugs can perform more than 30 consecutive jumps without tiring.<sup>1</sup>

It took the collaborative efforts of a team of 13 scientists from America and China to discover the secret to the beetle’s bounce. They used a number of advanced techniques to visualise and

measure the biological structures and power output of the insect’s jumping mechanism—micro-computed tomography (micro-CT scans), 3D computer reconstructions, high-speed filming, and light microscope dissection. The scientists measured the beetle’s jump, calculating its power and acceleration, and the figures derived are astounding! Regarding *Psylliodes punctifrons*, the authors report:

“The jump pushes individuals to a final velocity of  $5.58 \pm 0.5$  m/s. The peak instantaneous power output (per unit mass) calculated for the hind legs in this species was  $2.2 \pm 0.1 \times 105$  W/kg, which is approximately 449 times that of the fastest-known muscle ... and some 100–200 times that of a powerful rally car engine.”<sup>1</sup>

These startling statistics place these insects on the top podium, in terms of acceleration and power, of all known jumping insects, with second and third place going to fleas and leaf hoppers respectively.

## A spring in its step

The mechanism responsible for the beetle’s jumping prowess turned out to be a sophisticated spring (figure 1).

However, the authors of the paper fail to credit the Creator for the mechanism enabling these beetles’ dramatic locomotive abilities. Rather, they resort to empty platitudes that elevate evolution:

“... nearly all the species of flea beetles have an ability to jump and

this ability is commonly understood as one of the key adaptations responsible for its diversity.”<sup>1</sup>

Furthermore, *a priori* they resort to evolution to explain the specifics of the beetle mechanism: “Flea beetles have evolved an enormous independent spring to aid the storage of elastic potential energy.”<sup>1</sup> But such an evolutionary explanation for the origin of the beetle’s jumping mechanism begs the question as to how they survived before they evolved this ability; the leap of logic for evolution being that beetles that fail to escape predators don’t leave progeny, so their genes are not passed on.

The jumping mechanism, situated in the beetle’s hind legs, is made of three moving parts (a latch, trigger, and spring) attached to muscles. The jump sequence has four phases, each of which increases the angle of the femur compared to the tibia. Phase I (crunching): muscles in the tibia contract, causing the tibia to flex. Phase II (co-contraction): extensor and flexor muscles in the tibia contract simultaneously, catching a triangular plate (see figure 1 ‘F2’) and inhibiting the tibia from extending further. Phase III (triggering and acceleration): the triangular plate is dislodged, causing the explosive release of stored energy. Phase IV (relaxation): the flea beetle is explosively launched upwards and the tibia muscles return to their initial relaxed position.

Good designs are typically repurposed for other applications. It has been discovered that a similar spring-catch-trigger mechanism exists in the snapping jaws of the Dracula ant<sup>2</sup> and

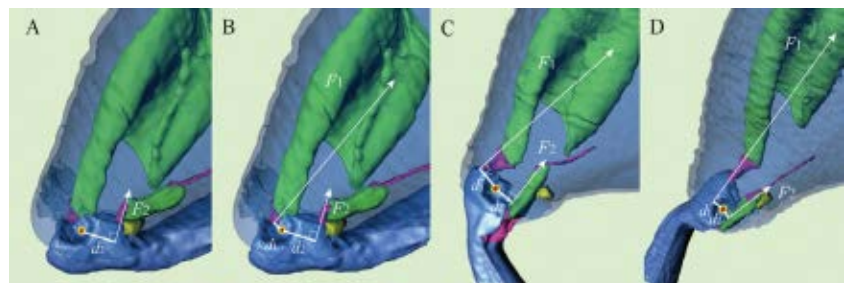
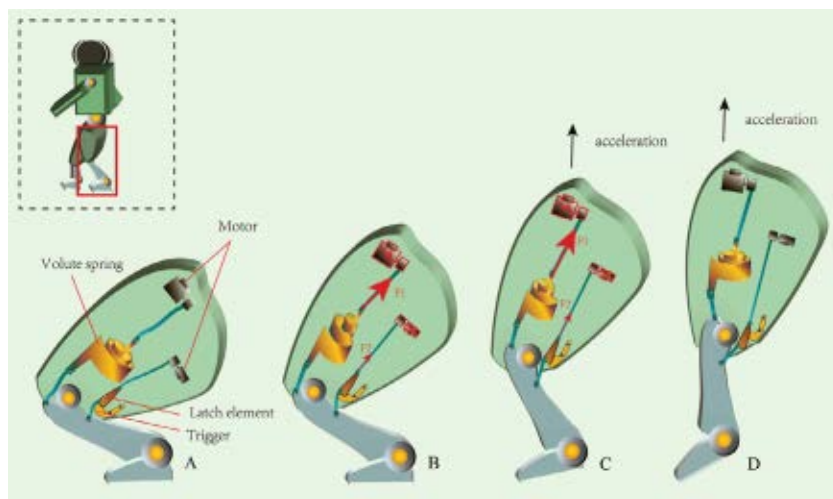


Figure 1. Dynamics of flea beetle hind leg catapult mechanism (figure 5 from Ruan Y. *et al.*<sup>1</sup>)



**Figure 2.** Robotic design of jumping limb inspired by flea beetle leg (figure 6 from Ruan Y. *et al.*<sup>1</sup>)

a four-bar snapping mechanism exists within the jaws of the snipefish (relatives of the sea-horses).<sup>3</sup> These kinds of apparatus give every appearance of being ‘irreducibly complex’ mechanisms. In other words, like Michael Behe’s mousetrap,<sup>4</sup> all the component parts of the beetle’s jumping mechanism have to be present for the system to function. It cannot be further simplified without complete loss of function. The catapult mechanism in these beetles relies on the perfect balance of specifically shaped parts and their elastic properties. But how this mechanism could have evolved in an incremental way is impossible to conceive. The structure would need to be complete to afford the beetle a survival advantage to begin with.

### Inspiration from creation

Inspired by the elegant jumping apparatus of flea beetles, the researchers proposed a robotic limb design (figure 2), using a similar mechanism. This section of their paper employs the term ‘design’ 12 times to describe the scientists’ robotic plan, itself based on their observations of the beetles. To produce such an engineering achievement, a great deal of planning and forethought must be applied—a far cry from the blind evolutionary processes

that they propose for its origins. How much more brilliant a construction was conceived by the Divine Designer of the beetle, which the clever scientists tried to emulate?

### Insect design

The spring apparatus of flea beetles is just one of many brilliant insect designs that have inspired engineers. Another example of an irreducibly complex jumping mechanism is the interlocking gear system discovered in nymph-stage leaf hoppers, the gears functioning as mechanical regulators for the insect’s jump.<sup>5</sup> Gear systems, by their very nature, are irreducible, necessitating many integrated parts, each of specified complexity. These natural systems exhibit all the hallmarks of intelligent, engineering design. Conversely, these same structures are to be seen in the earliest fossils,<sup>6</sup> demonstrating that there is no evidence of evolution.<sup>7</sup> Evolution cannot account for what is observed in nature in terms of its information and complexity.<sup>8</sup>

### Summing up the science

The flea beetle jumping mechanism discussed here can be added to an increasing list of ‘irreducibly complex

mechanisms’ found in nature.<sup>9</sup> Such systems are completely dependent upon each of their specific components for the mechanism to work correctly (or at all). Remove one component and the function of the whole is lost. This is axiomatic of human engineering systems, which require all their separate parts to function together. Intelligently created machines exhibit specified complexity, and require forethought and problem solving for their manufacture. This is as true for the robotic leg design as it is for the beetle design which inspired it.

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# 'Snowball Earth' out with a bang?

Edward Isaacs

Ever since the discovery that Earth had once been glaciated to a far greater extent than it is today, the Ice Age has been an iconic feature of secular geology. Although a single ice age in the recent past challenged the notion of uniformity of Earth's gradual processes, the uniformitarian multiplication of Earth's glacial periods was quickly heralded as a victory for the antiquity of Earth, despite the evidence supporting a single glaciation.<sup>1</sup> Over the succeeding decades, geologists have inferred dozens of alleged glaciations, predominately in five major periods of geohistory (table 1), the oldest of which are the Huronian glaciations (2.45–2.22 Ga) in the Early Proterozoic.<sup>2</sup> These

Huronian glaciations, among others, are opined to have been uncommonly extensive, dominating the majority of Earth's surface, even to the equatorial regions. Popularly termed 'snowball Earth', this inference has nearly gained consensus in secular geology and great repute in the entertainment sector. Notwithstanding this popularity, numerous challenges plague these uniformitarian notions, chief of which is the lack of a melting mechanism to end the perpetuation of these global ice ages. In a desperate attempt to save the paradigm, a recent study has suggested that an asteroid impact terminated the Huronian glaciations (figure 1).

## The old story

Beginning in the mid-nineteenth century, geologists began recognizing evidence for a glaciation in recent geohistory that far exceeded the present glacial extent. Following the trend to minimize the influence of the Genesis

Flood, some geologists heralded the discovery of an ice age as accounting for the surficial deposits ('diluvium') previously relegated to a diminutive Genesis Flood, allegedly eliminating the need for a Flood-based geology. Although the presence of an ice age challenged uniformitarian doctrine ('the present is the key to the past'), geologists soon inferred other supposed glaciations throughout geohistory that coincided appropriately with the cyclicity of gradualistic geology. These cycles of glacial and interglacial alternations have been identified in five major periods of Earth's history, the earliest being the glaciations of the Early Proterozoic. These early ice ages, equalling three discrete glacial periods between 2.45–2.32 Ga, and possibly a fourth ending at 2.2 Ga (the Makganyene Glaciation<sup>3,4</sup>), have been termed the 'Huronian glaciations' based on the initial identification of 'tillites' (alleged lithified glacial deposits) in Southern Canada.<sup>2</sup> Paleogeographic reconstructions suggest that these supposed tillites formed along the equator, indicating that glaciations had dominated the majority of Earth's surface in the Early Proterozoic. This has resulted in the popular sobriquet 'snowball Earth' for these and other similarly pervasive glaciations.<sup>5</sup>

Despite the overwhelming consensus, numerous challenges continue to plague these alleged ancient glaciations. Much of the diagnostic criteria used to identify ancient ice ages can be explained by mass wasting;<sup>6</sup> even the initiation (and thus the cyclicity) of an ice age is wholly inexplicable in secular geology.<sup>7</sup> Snowball Earth particularly lacks a forcing mechanism to end an ice age. Such an extensive glaciation would produce such a high reflectivity (albedo) that it would be nearly impossible to heat Earth out of a glaciation, especially during a time when solar irradiance was greatly diminished.<sup>8</sup> To account for these challenges, numerous rescuing mechanisms have



Image: Rafael Moura Sb/Pixabay

**Figure 1.** The naturalistic paradigm of multiple ice ages has long been plagued by a lack of a plausible mechanism for initiating glaciation, and, in the case of those glaciations allegedly near global in scale, a failure to explain their cessation. A recent study claims that the Huronian 'snowball Earth' glaciations were terminated by an asteroid impact, but rather than solving the dilemma of heating Earth out of a perpetual global glaciation, the study merely confirmed the obvious: the naturalistic paradigm of multiple ice ages is doomed.



been proposed, including an increase in volcanism accompanied by an influx of greenhouse gases, although this also suffers from major difficulties.<sup>9</sup>

### A new twist

Faced with these insurmountable challenges, what can secular geologists do? Following the resurgence of naturalistic neocatastrophism in recent decades, a greater number of secular geologists have begun to rely on extra-terrestrial forcing mechanisms, as did Ericson *et al.* in their recent Goldschmidt abstract<sup>10</sup> and paper in *Nature Communications*.<sup>11</sup> After investigating the Yarrabubba Crater of the Australian Outback, Ericson *et al.* proposed that an asteroid impact strengthened the termination of the global Huronian glaciations (figure 1).

Located in the Archean Yilgarn Craton of Western Australia, the Yarrabubba Crater is replete with shatter cones, pseudotachylytes,<sup>12</sup> and other diagnostic criteria that confirm it as one of the largest impact craters in the area and it has been dated as among the oldest along the craton,<sup>13</sup> if not the world.<sup>11</sup> Despite the evidence for an impact, the granitoids and greenschists that harbour this impact structure have made dating this site anomalous. Early research by McDonald *et al.* suggested an upper limit of 2.65 Ga, based on the interpretation that the Barlangi Granophyre was an impact melt,<sup>14</sup> although later researchers preferred 1.1 Ga, based on pseudotachylyte dikes.<sup>13</sup> Upon this groundwork, Ericson *et al.* dated the impact to no more than about 2.6 Ga, as calculated by McDonald *et al.*, but preferred a date of 2.2 Ga. This younger age roughly coincides with the end of the Makganyene Glaciation, the finale of the Huronian glaciations at 2.22 Ga.<sup>2</sup> Ericson *et al.* opine this impact melted a considerable volume of ice and ejected it into the atmosphere. This would allegedly lower the cumulative albedo of the

terrestrial cryosphere while increasing the atmospheric levels of water vapour, producing a greenhouse warming and thus ending the Huronian glaciations. It was not long before the Ericson *et al.* proposal began gaining attention from the popular media for its allegedly novel solution to snowball earth, including an article in *Science*.<sup>15</sup>

### Challenges galore

A common consideration, particularly for those skeptical of an impact inducing the End Cretaceous mass extinctions,<sup>16</sup> is that coincidence does not necessitate causation. However, age estimates of the local geology ranging from 2.65 to 1.1 Ga make it hard to even show that the Yarrabubba impact was coincident with the cessation of the Huronian glaciations. Such a wide array of possible dates should caution researchers against possibly forcing the numbers, but even so the termination of the Huronian glaciations is subject to much debate,<sup>17</sup> making it impossible to prove coincidence.

Even if the Yarrabubba impact was indeed coincident with the end of the Huronian glaciations, the impact would merely correlate to the Makganyene Glaciation, the final of four distinct Huronian glaciations. If the preceding three glaciations could be terminated

without impacts, why is an impact required to end the fourth glaciation? Even so, the Makganyene Glaciation is the most tenuous and debated of the four, as it has been discovered only in southern Africa<sup>18</sup> and possibly China.<sup>19</sup> So little is known about this ‘glaciation’ that secular geologists must infer a minimum age of 2.2 Ga, based on dating flood basalts which unconformably overly the alleged tillites,<sup>3,20</sup> allowing a date greater than 2.2 Ga to be acceptable. How difficult it is to prove coincidence between two events, the dates of which are not known!

Computer simulations in the Ericson *et al.* paper suggested a variety of climatic responses to the impact, most of which indicated only minimal response. Unlike the optimism of Ericson *et al.*, some scientists doubt that enough ice could be melted and ejected into the atmosphere to initiate the necessary greenhouse effect.<sup>15</sup> Even if adequate quantities of liquid water could be introduced into the atmosphere, the Yarrabubba impact produced extensive ejecta that would raise aerosol levels in the stratosphere. Having a high albedo in their own right, these aerosols would quickly become nucleation sites for the newly melted water in the atmosphere. Because cool air can retain little water before reaching the dew point, this newly melted water could not be long

**Table 1.** Secular geologists postulate that Earth has undergone five major glacial phases. Glaciations of both the Early Proterozoic (Huronian glaciations) and Neoproterozoic are thought to have been global in scale, leading to their vernacular sobriquet ‘snowball Earth’. Compiled from Crowell.<sup>21</sup>

Geological Period	Approximate age range
Pleistocene	11,700 ka to 2.6 Ma
Late Paleozoic	256 to 338 Ma
Late Ordovician–Early Silurian	429 to 445 Ma
Neoproterozoic	520 to 950 Ma
Early Proterozoic	2.2 to 2.4 Ga



retained in the cool, dry atmosphere of the snowball earth climate before condensing. These resulting clouds, known to meteorologists as some of the most influential thermostatic regulators in the atmosphere, would merely equalize the greenhouse effect by reflecting incoming solar radiation, which would have been lower due to the faint young sun paradox.<sup>8</sup> Rather than commencing a runaway greenhouse effect, these factors could initiate a negative feedback mechanism that would soon terminate any net heating introduced by the Yarrabubba impact.

## Conclusions

Ever since the discovery of the Ice Age, uniformitarian geology continues in vain to understand this unparalleled phenomenon. Although cyclic glaciations may better coincide with uniformity, repeated ice ages only multiply the challenges. To remain internally consistent with the application of their diagnostic criteria, the uniformitarians are compelled to postulate global glaciations despite the various difficulties. Oddly enough, secular geologists seem more than content to propose global inundations of ice but abhor any suggestion of a global flood!

The lack of a forcing mechanism to end snowball Earth leads to the production of such *ad hoc* suggestions as an inexplicable increase in volcanism or a mystifying influx of atmospheric greenhouse gasses. The asteroid impact of Ericson *et al.* suffers a similar fate. Not only is causation impossible to demonstrate, but even the coincidence of the impact with the end of the final Huronian glaciation is dubious. Rather than terminating a glaciation, an impact may even reinforce the glaciation by adding highly reflective ejecta and aerosols into the atmosphere and producing high albedo clouds. The Ericson *et al.* study also neglected the effects of the lower levels of solar irradiance due to the faint young sun paradox. Indeed, instead

of solving the mystery, Ericson *et al.* merely reinforced the reason for doubting the multiple ice age paradigm. Because of the failure of uniformitarian postulates, some secular researchers continue to search for a causal forcing mechanism to terminate the Huronian ‘snowball Earth’ glaciations. As long as the impact of the Genesis Flood on our planet is ignored, the Ice Age will remain a baffling puzzle to secular researchers.

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# Colonial nesting or hurried egg laying by dinosaurs?

Michael J. Oard

Uniformitarian scientists often observe features that are difficult to explain in their paradigm. However, they interpret them by adding secondary hypotheses because of their allegiance to uniformitarianism and evolution. They do this without evidence, adding interpretations that go beyond the data. It can be difficult to spot their creative (and fanciful) solutions, especially when we are not privy to all the data. For instance, a recent report of egg clutches found in the Javkhland Formation in the eastern Gobi Desert of Mongolia.<sup>1</sup>

## The observations

Millions of dinosaur eggs are found in sedimentary rocks all over the world. They are often found in clutches (figure 1). In the Gobi Desert, Tanaka *et al.* observed eggs in at least 15 clutches with 3 to 30 eggs in each clutch with no discernible arrangement.<sup>1</sup> Half of the area has been eroded, so it is likely there once were twice as many clutches. The egg clutches were found on top of a common paleosurface of sandy, light gray mudstone. Sometimes they were bunched up with the shortest distance apart less than 1.5 m and an average of one clutch per 10 m<sup>2</sup>. The clutches cover an area of about 286 m<sup>2</sup>. The eggs had an average diameter of 13 cm with a range of 10–15 cm, and the shells were an average of 1.55 mm thick and very porous. The upper part of many of the eggs has been lost to modern erosion.

The scientists observed that the sediments within the eggs consisted of two distinct layers: (1) a lower, dull orange, sandy mudstone 3–5 cm thick, and (2) an overlying, red very sandy mudstone 1–6 cm thick. Each layer was fining upward, as if laid in a current. Above the red mudstone, the dull orange mudstone continued, both of which were laterally extensive. The upper red mudstone layer contained mud clasts, pebbles, volcanic fragments, and caliche pebbles, also found in the gray mudstone below the eggs. The caliche is interpreted as pedogenic.

## The faulty uniformitarian interpretations

The scientists claim that the area is a colonial nesting area of likely therizinosauroid theropod dinosaurs. The egg clutches were said to be nests that were fully covered and incubated by the dinosaurs:

“Although no sedimentological evidence indicative of nest structure was found associated with the Javkhland clutches, statistical methods were used to infer nest type (i.e. covered versus open). Based on a linear discriminant analysis between egg mass and eggshell porosity in

extant archosaurs (Tanaka *et al.*, 2015), the high porosity of the Javkhland eggs (646 mm porosity for an egg mass of 1204 g: see the Data Repository) indicates they were incubated in fully covered nests.”<sup>2</sup>

The scientists are weaving a story around the observations that the eggs were laid on a generally flat paleosurface and that they are highly porous. There is no indication the eggs were covered by soil or vegetation or placed in a hole, or that the clutches were nests. The few dinosaur nests that are found indicate that the eggs would be laid in a dug out hollow with sediment piled upon the sides, as observed on ‘Egg Mountain’, Montana, USA. In fact, there are very few nest structures associated with the numerous dinosaur eggs found anywhere in the world.<sup>3</sup> Uniformitarian scientists usually infer a nest by the presence of an egg clutch:

“Despite the relative abundance of dinosaur eggs in the fossil record (Carpenter *et al.*, 1994; Carpenter, 1999), trace-fossil evidence of dinosaur nest construction is extremely rare. The existence of a nest is typically inferred by the presence of an egg clutch and usually it is not



**Figure 1.** A lambeosaurine, duck-billed dinosaur egg clutch found in north-central Montana, USA, and displayed at the Museum of the Rockies, Montana State University, Bozeman, Montana



accompanied by physical evidence of nest architecture.”<sup>4</sup>

Chiappe *et al.* probably feel free to admit this because they think they found six more nests in Argentina. However, these candidate nests are likely dinosaur tracks.<sup>5</sup> There is little or no evidence for dinosaur nests, and it is simply an *ad hoc* uniformitarian interpretation based on the fact that most dinosaur eggs are very porous, similar to reptiles.<sup>6</sup>

Furthermore, little evidence exists that dinosaur eggs were covered with vegetation to keep them warm and moist:

“The suggestion that some dinosaurs may have nested in vegetation or vegetation-mud mounds similar to those of megapode birds or alligators seems to be a popular idea ... but how can this be proven when all traces of vegetation have rotted away? Or how can we determine if vegetation was even used at all?”<sup>7</sup>

Admitting the traces of vegetation are rare, the idea it rotted away is contradicted by a lack of pollen evidence and the continued existence of delicate dinosaur eggs or shell fragments.

Moreover, it is claimed that the sediments were pedogenic, mainly because of the caliche particles, so the clutches were believed to have been incubated in a soil or organic rich substrate.<sup>2</sup> However, the caliche particles could have simply been eroded from a carbonate layer, since there were other indications of erosion such as mud clasts, pebbles, and volcanic fragments. The soil and organic-rich substrate is an inference that appears to have little or no evidence.

The scientists also claim that many “had hatched eggs before the site was buried by flooding.”<sup>2</sup> This was because randomly orientated openings in the upper half of the egg from the clutches are reminiscent of a hatching window made by a hatchling escaping the egg. Eggshell fragments up to 6 cm in diameter, similar to the opening in the

eggs, were found *inside* some of the eggs, and eggshells scattered around two clutches. But why would a large eggshell fragment be found within the egg if the hatchling pushed the shell outward? Four clutches not only had open tops but also the red marker bed visible inside, indicating that the eggs were open at the time the upper layer was deposited. Nine clutches had at least one egg that is believed to have hatched, similar or greater than the success of crocodiles and some birds. However, no hatchlings were found. The idea of hatching dinosaur eggs is thus an inference. There are other possibilities, besides hatching, such as erosion by currents and scavenging by predators. The authors list several potential predators found in the Javkhant Formation, such as turtles, lizards, other theropods, and eutherian mammals.<sup>1</sup>

The inference that the eggs were all laid at the same time is a good deduction because of the two layers of mudstone in the eggs. However, the authors take this too far because of their belief in evolution:

“When considered in an evolutionary context, this study supports the idea of a gradual acquisition of avian reproductive traits through theropod evolution ... although widespread among living birds, nest attendance/protection behavior among colonial nesters appears to have first evolved in non-brooding non-avian dinosaur species.”<sup>8</sup>

The fact that these clutches are concentrated also indicates that these egg clutches were laid at the same time, but they extrapolate by imagining that this was the beginning of brooding, colonial nesting. Interestingly, the remains of the mother dinosaurs are absent, but they still believe that the dinosaurs must have attended and protected the nests for a while. So, the idea of brooding and nest protection is another unfounded uniformitarian, evolutionary inference.

## A BEDS alternative origin

The evidence better supports the BEDS (Briefly Exposed Diluvial Sediments) model during the Flood.<sup>9</sup> The evidence indicates that the Gobi Desert eggs were laid on flat bedding planes, as are most other dinosaur egg clutches. It also indicates hasty egg laying since there seems to have been no time for nest construction. The area of exposed sediment must have been small, which explains why so many theropods laid their eggs close together. The authors admit that the eggs were buried in a flood. Although they automatically think it is a local flood because of their assumptions, it could easily have been continued flooding after sediments were briefly exposed in the Genesis Flood.

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# Do five dropstones define another Proterozoic cold period?

Michael J. Oard

There are three main diagnostic indicators used to support ancient ice ages<sup>1</sup> that are supposedly hundreds of millions to billions of years old.<sup>2</sup> These indicators are striated and faceted rocks, striated bedrock, and dropstones in varvites. Faceted rocks have been ground down by friction to a flat surface, presumably by glacial movement. A dropstone is a rock that is larger than the containing layers, while varvites are believed to be lithified varves—rhythmites believed to have been laid down in one year. Rhythmites are regularly repeating laminae of two or more lithologies. Striated bedrock is solid rock typically underlying unconsolidated surface materials that has small (often parallel) grooves scratched into its surface.

Varves form today in lakes and are often composed of silt (summer) and clay (winter) laminae. However, it is known among some geologists that rhythmites can be duplicated by other processes, such as mass movement (see below).<sup>3,4</sup> Unfortunately, many geologists, when they find dropstones in fine-grained sediments, simply assume glaciation is the cause, or at least that sea or lake ice picked up rocks from near the shore. They assume glaciation depending on the age of the enclosing rocks.

## Lonestones in thin-bedded sediments

Based on just five dropstones found in lithified fine-grained sedimentary rocks, several geologists added another cold period within the Neoproterozoic.<sup>5</sup> The outcrop is dated as very early Neoproterozoic at little less than 1000 Ma,

near the Mesoproterozoic and Neoproterozoic boundary. Although the stones were found in northwest Scotland, the paleolatitude is thought to be 35°S.

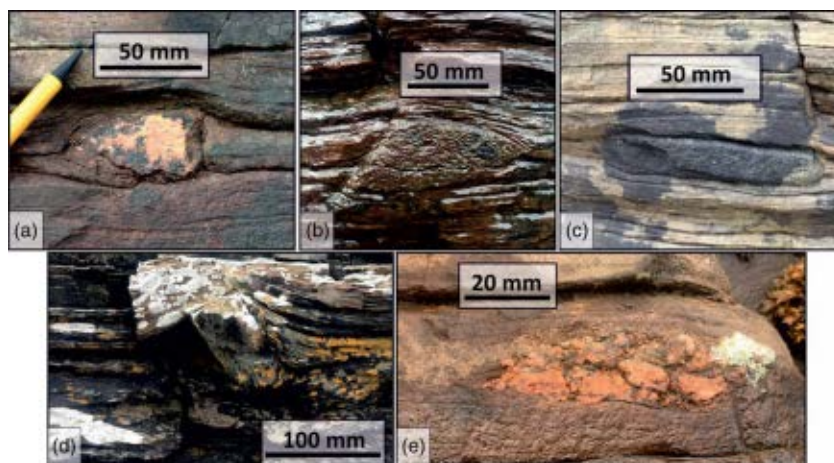
The dropstones are isolated and restricted to a single horizon over a distance of 250 m. Therefore, the dropstones should be called ‘lonestones’, because they are isolated within the formation. The lonestones are from the Lewisian gneiss basement with amphibole dykes that outcrop close by. They are small (around 3.5–9 cm long), and so are easier to incorporate in fine-grained sediments by some mechanism other than by being dropped. Four of the lonestones are parallel to bedding and one forms a 60° angle (figure 1). Hartley *et al.* list four possible mechanisms of emplacement: biological rafting, flotation, ice rafting, and projectiles. They miss other mechanisms, such as swimming animals, waterspouts, and mass movement. Because they believe in evolution, they eliminate biological rafting and swimming animals. They propose ice rafting, since they believe in Proterozoic ‘ice ages’. They do briefly discuss mass movement, but eliminate it because they think the strata should be comprised of more coarse-grained sediments, which is not necessarily true. Debris flows can be mudflows and can carry outsized clasts.

So, they conclude the lonestones were dropped from ice, and as their proof they point to the deflection and penetration of the layers. It appears from figure 1 that only two lonestones, (a) and (d), have deflected the layers below, as if they were dropped.

The layers were not considered varves but thin-bedded ancient lake sediments. The scientists determined that the lonestones must have been dropped from lake ice because there is no other evidence of glaciation. Besides, there is not supposed to have been a major glaciation at about 1,000 Ma. The Neoproterozoic has about three (supposed) global or nearly global glaciations, but all are ‘dated’ younger than 700 Ma.<sup>6</sup> Another reason is its relatively low paleolatitude of 35°S, but even for lake ice to form, the location must have been at high altitude. So, the authors deduce at least another Proterozoic cold period.

## A Flood mechanism alternative

More explanations for these lonestones are possible within the Genesis Flood framework. Creation scientists are divided on the location of the pre-Flood/Flood boundary and the location of the Mesoproterozoic and Neoproterozoic in sedimentary rocks within biblical Earth history. Some think Proterozoic sedimentary rocks are pre-Flood,



**Figure 1.** The five lonestones in fine-grained layers.<sup>26</sup> Note the deflection of laminae above and below the clasts in (a) and (d) and the variations in size, shape, and composition. Figure 1 (c) looks like a concretion, but it is an igneous rock and therefore a lonestone.



Creation Week rocks, or early Flood rocks deposited in basins and rifts. More research is needed. I prefer the latter possibility and have given reasons why I think it is likely that Proterozoic sedimentary rocks are from the very early Flood.<sup>7–9</sup>

Just because the beds are thin, it does not mean they are from a lake. In the Flood and even in a uniformitarian model, thin-bedded layers can form by turbidites and hyperconcentrated flows that leave numerous rhythmites. Hyperconcentrated flows are flows that contain 40–80% by weight of sediment in water, which is intermediate between turbidity currents with less sediment and debris flows with more sediment.<sup>10</sup> Many rhythmites can form in one year by several different mechanisms, such as turbidites.<sup>11</sup> In today's climate, numerous varve-like rhythmites are being formed in one year in Muir Inlet, Alaska, after glacial retreat.<sup>12</sup>

The two limestones that disrupt the layers in figure 1 probably were dropped, and it is possible all five were dropped and would be real dropstones. However, that does not mean ice had anything to do with their emplacement. The limestones could have been dropped from a floating log, kelp, or from stomach stones from swimming animals.<sup>13</sup> These were eliminated by the authors of the report because they do not believe kelp, logs, or swimming animals existed in the Proterozoic. But, in a Flood model, all would have existed from the very beginning of the Flood. The fact that all five rocks are found on one horizon could mean a sudden drop from the roots of a tree or from kelp that lasted only a short time, or it could mean sudden horizontal emplacement in a mass flow. If the rocks were dropped by lake ice, from kelp, or from floating logs, why are there so few and none in the many more horizons of the hundreds-of-metres-thick formation? During the early Flood, where sediment is being deposited rapidly, it is more likely that the limestones were deposited by mass flow.

Disrupted layers below a stone are not necessarily indisputable proof of a dropped stone. Owenshine states:

“Unfortunately, penetration and deformation of strata below an iceberg-rafted stone may be very slight (Hardy and Legget, 1960), absent, or *indistinguishable from the later effects of compaction*. ... Thus there are ambiguities in determining whether iceberg rafted components occur in a particular sedimentary section [emphasis added].”<sup>14</sup>

So, the limestones could have been emplaced by mass movement, especially turbidity currents and hyperconcentrated flows that leave rhythmites. Schermerhorn states: “scattered stones in laminated or massive sediments need not have been dropped in but may have been emplaced by later transport.”<sup>15</sup> Others support Schermerhorn's deductions:

“Many turbidites appear to contain floating megaclasts, ... Reported examples include the deposits of inferred high-density turbidity currents that contain isolated, floating megaclasts up to a few decimetres or even a few metres in their long dimension.”<sup>16</sup>

In the early Flood, massive tectonics, strong turbulent currents, and the shattering of rocks would be expected in many areas.<sup>17</sup> Eroded rocks from the Lewisian gneiss from the edges of 600-m-deep paleovalleys in the gneiss could have added limestones to fine-grained sediments by turbulent plucking. The rocks then could have fallen through sediment-filled water until they came to rest at the bottom.

There are many instances of dropstones in thin-bedded strata that are not associated with glaciation or no longer glaciogenic, such as the Cretaceous of South Australia in which dropstones up to 80 cm were found in massive to laminated silt.<sup>18,19</sup> Many claimed glacial deposits defined by dropstones in thin-bedded sediments have been reinterpreted as mass flow deposits; for instance, the so-called glacial deposit in northern Norway.<sup>20,21</sup> The classic dropstone varvite supporting the 2.2-Ga-old

glaciation in the Gowganda Formation was interpreted to be a distal turbidite by Miall.<sup>22</sup> Presumed Neoproterozoic glacial deposits based on dropstones in fine-grained sediments were reinterpreted as the product of subaqueous mass flow.<sup>23</sup> Dropstones in fine-grained sediments are reported from tropical environments as well as many other non-glacial environments.<sup>24</sup> Other instances are reported in the scientific literature.<sup>25</sup>

## Conclusion

The five limestones found in the very early Neoproterozoic in northwest Scotland do not necessarily indicate they were dropped, or that the thin-bedded layers were lake deposits. Several mechanisms form dropstones in fine-grained layers. The limestones need not be dropped by lake ice, suggesting another Proterozoic cold period. There are other interpretations, especially considering the Flood and mass flow.

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## Uniformitarian scientists claim 'snowball Earth' caused the Great Unconformity

Michael J. Oard

Uniformitarian scientists often force themselves into an intellectual trap when they must fit their previous assumptions and conclusions into a coherent whole. For instance, the uniformitarian dating of deep-sea cores has led uniformitarians to believe that glacial/interglacial oscillations of the past 900 ka oscillated every 100 ka. This was proposed so they could harmonize the cores with changes in the eccentricity of the earth's orbit. However, the Milankovitch cycle produces extremely little change in total, hemispheric, or seasonal solar radiation on the earth.<sup>1,2</sup> But they are stuck with the 100 ka cycle. As a result, uniformitarian, aka secular scientists have been vainly searching for some kind of boosting mechanism for almost 50 years. Another trap for secular scientists is the idea that snowball Earth, part of their pre-Pleistocene 'ice ages', somehow carved the Great Unconformity.

### Snowball Earth challenges uniformitarianism

The 'snowball Earth' idea proposes the earth was totally or almost totally glaciated at times within the Proterozoic, 2.5 billion (Ga) to 542 million (Ma) years ago in the uniformitarian geological timescale.<sup>3,4</sup> Proterozoic ice ages, as well as Paleozoic ice ages, are based on finding glacial till-like rocks and other features within sedimentary rocks, thought to be diagnostic of glaciation.<sup>5,6</sup> Many of these supposed

ice age deposits in the Proterozoic are found at low paleolatitude, based on paleomagnetism, and are marine. Thus, secular scientists have been *forced* to conclude that the earth was totally glaciated or mostly so several times in the Proterozoic. One was in the early Proterozoic, or Paleoproterozoic.<sup>7,8</sup> The number of Earth-covering glaciations in the Neoproterozoic has been debated, ranging from possibly four,<sup>9</sup> three,<sup>10</sup> or two.<sup>11</sup> Keller *et al.* believe the Sturtian ice age (717–660 Ma) and Marinoan ice age (641–635 Ma) were global while the Gaskiers ice age (~580 Ma) was almost global.

The snowball Earth idea has raised two major challenges for secular scientists because they insist that practically all the till-like rock deposits were formed by glaciation. First, with a snow-covered surface, the earth would probably cool 100°C<sup>12</sup> due to the high reflectivity (albedo) of snow and the lack of heat sources (other than the sun). Second, some outrageous hypothesis is needed to melt the snow and ice, and do it at a time when solar luminosity was 10–30% less than it is today. The weak sun is due to their adherence to the big bang 'theory' which starts out with a faint sun.<sup>13,14</sup> One proposal to melt a glaciated earth is for CO<sub>2</sub> to increase 50–225 times,<sup>15,16</sup> although these figures are disputed.<sup>17</sup>

Some secular scientists have suggested alternative hypotheses for the glacial-like features, such as mass flow for the Proterozoic 'ice age' features,<sup>18</sup> and I believe they are correct.<sup>5</sup> These Proterozoic, as well as Paleozoic, deposits, some of which are the size of the state of Texas, USA, can readily be explained by gigantic submarine mass flows during the earliest stages of the Flood.<sup>5,19</sup>

### Snowball Earth claimed to be the cause the Great Unconformity

As if the problems from the hypothesis of snowball Earth are not enough, several secular scientists also claim



that snowball Earth eroded an average of 3,000–5,000 m of rock from the earth's surface to produce the Great Unconformity!<sup>20</sup> The Great Unconformity is an erosional surface often observed on igneous and metamorphic crystalline rocks of the upper crust and/or Precambrian sedimentary rocks deposited in deep basins. The Great Unconformity is a nearly flat surface but does have a little relief in places, which is why it is called an erosional surface and not a true planation surface. It is found near the bottom of the Grand Canyon in northern Arizona, USA,<sup>21</sup> and surprisingly at the tops of the mountains in parts of Wyoming and Montana.<sup>22</sup> In the Beartooth Mountains of Wyoming and Montana, the Great Unconformity has been faulted to different altitudes, up to over 4,000 m above mean sea level. It has been partially eroded in some areas, but is still observable (figure 1).

It is likely the Canadian Shield (at least in part), where most Phanerozoic sedimentary rocks are missing, based on erosional remnants of mostly Paleozoic sedimentary rocks, represents a huge exposure of the Great Unconformity. It is claimed that portions of the Canadian Shield experienced about 5,000 m of erosion mostly during the Neoproterozoic, deduced from the exposure of the lower portion of the Sudbury Impact Structure in Ontario, Canada.<sup>23</sup>

The Great Unconformity is considered global in extent, but highly diachronous (i.e. thought to have been formed at different times) and likely not one large erosion surface on each continent:

“While nonconformity between sediment and crystalline basement is ubiquitous on all the continents, it is highly diachronous (6). This diachroneity of amalgamated unconformities has helped to obscure the global significance of Neoproterozoic glacial erosion.”<sup>24</sup>

Thus, uniformitarian scientists conclude that the Great Unconformity



**Figure 1.** The top of the Beartooth Mountains in south-central Montana showing the Great Unconformity cut flat on granite and gneiss of the upper crust. The erosion surface has been faulted upward to various altitudes, while the portion in the foreground has been roughened by erosion.

is likely more a series of local-to-regional unconformities on each continent with anywhere from 200 Ma to over 2 Ga of time missing from the generally flat-lying sediments on top.

Indeed, the Great Unconformity is a major mystery for uniformitarian scientists:

“The Great Unconformity, a profound gap in Earth’s stratigraphic record often evident below the base of the Cambrian system, has remained among the most enigmatic field observations in Earth science for over a century.”<sup>25</sup>

One of the most perplexing observations is that the Great Unconformity is *not* associated with any tectonic event, like other unconformities in the rock record: “Erosional unconformities are common throughout the geological record and often have a plausible tectonic cause.”<sup>26</sup>

Secular scientists throw in several hundred million to a few billion years to explain how snowball Earth could have eroded thousands of metres of rock. They claim glacial erosion must have been variable with ice sheets that ranged from very thin to 6,000 m thick. Most of the ice movement is

attributed to surface slope. Nonetheless, the ice sheets had to be exceedingly active to erode 5,000 m of rock. It is not realistic for ice to build to a thickness of 6,000 m, since the thicker the ice sheet becomes, the colder and drier the climate would also become, and the more it would distance itself from a moisture source. Moreover, an ice and snow cover would produce colder temperatures by snow/albedo reinforcement: the more fresh snow the colder the temperatures would become. When temperatures continue to fall well below freezing, the air can hold less and less moisture. It soon becomes ‘too cold for snow’, as they say in the far north.

The authors of the paper on snowball Earth suggest that sublimation, in which the ice ‘evaporates’ could provide the necessary moisture.<sup>10</sup> But as temperatures of the atmosphere plunge toward  $-100^{\circ}\text{C}$ , especially with much less solar radiation due to the faint ‘young’ sun, it is doubtful significant sublimation could occur. Besides, sublimation is taking from the snow and then redepositing it for no net gain.

And of course there is the problem that as snow and ice spread

everywhere, it would quickly become cold-based and frozen in place, and therefore non-erosional.<sup>26</sup> Interestingly, according to the hypothesis late Proterozoic snowball Earth melted for short periods of time—three times! And all of this occurred from 717 Ma to around 580 Ma when life was supposedly evolving just prior to the Cambrian explosion.

The authors then go on to ask: where did all the sediments from 5,000 m of continental erosion go? The sediments ended up in the oceans, they say, but then all disappeared by subduction,<sup>26</sup> conveniently leaving no record and also no proof that their hypothesis is tenable.

### Creation science implications

The idea that snowball Earth could even occur and that it could erode an average of 3,000 to 5,000 m of rock shows just how easily secular scientists can box themselves into a corner because of their paradigm. The faint young sun should have produced snowball Earth for the entire Proterozoic and all but the early Archean, when the earth was supposedly hot. These should be fatal paradoxes to the evolutionary/uniformitarian worldview. This all goes to show that another explanation is more plausible: God's account of Creation and the Flood (Genesis 1–11).

More specifically, the evidence for ancient glaciations can be better explained by submarine mass flow during the Flood.<sup>5</sup> There was no time in the past that the sun was faint because there was no Big Bang and no billions of years. The Great Unconformity indeed does represent great erosion that occurred early in the Flood, but how much erosion is unknown. Such erosion could easily have happened at the beginning of the Flood when it was dominated by tsunami-like currents, very heavy rain, and powerful turbulence.<sup>27</sup> After the initial catastrophism of the Flood, sediments were

rapidly deposited on the Great Unconformity during the *Great Deposition*.<sup>28</sup> After most of the Flood sediments had been deposited into fossil-rich layers, sometimes thousands of metres thick, the majority of the world's mountains and even portions of the continents rose and the adjacent valleys sank, including the ocean basins late in the Flood year. Powerful tectonic forces helped to cause the Floodwater to drain into the oceans.<sup>29,30</sup> Global uplift of the mountain ranges at the end of the Flood explains why the Great Unconformity is now residing at the tops of the mountains, including those in southern Montana and Wyoming. The big picture of geology agrees with the biblical record.

### Acknowledgments

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# Fake evidence: and it's not in politics

***Fake Evidence: A look at evolutionary evidence for over 90 years in the court cases from Scopes to Kitzmiller***

Ron Milliner

HarperCollins, Nashville, TN, 2018

Jerry Bergman

Former science teacher Ron Milliner documents the fact that much of the evidence used to support evolution presented during the recent American creation–evolution trials is wrong or, at best, very problematic. He begins by reviewing the Scopes trial (1925), now one of the best-known court cases in American history (figure 1). As an illustration of its notoriety, the movie, based on a play about the Scopes Trial, *Inherent the Wind*,<sup>1</sup> was rated number two in a recent list of the *Five Best Movies on Science and Religion*, compiled by National Public Radio (p. 14).

Milliner shows that all of the arguments that evolutionists used in the Scopes trial testimony are now recognized as erroneous, including vestigial organs, the Piltdown man, and the ontogeny–phylogeny arguments of Ernst Haeckel. The scientists' vestigial organ argument as part of the Scopes trial was as follows:

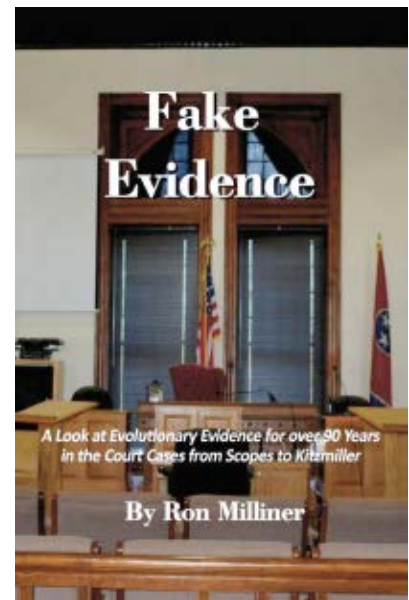
“There are in man, for example, very many structures of no conceivable present use, but showing resemblance in every other animal which are useful. The appendix vermiformis is one structure” (pp. 18–19).

The over-100 examples of other vestigial structures have now been fully refuted by the peer-reviewed scholarly journals.<sup>2</sup>

Those testifying in the Scopes trial included several of the leading scientists of the time, including University of Chicago anthropology professor Fay-Cooper Cole and Johns Hopkins University zoology professor Maynard Mayo Metcalf, the latter of whom was the only professor to testify on the stand. The rest of the scientists had to submit their testimonies in writing. These were then read into the trial record for the appeal, which the ACLU knew was the next step to achieving their goal. Their plan was to ensure that only evolution was taught, while all evidence against evolution, called ‘back-door creationism’, was not (p. 16).

A scientist's testimony being read into the record was to the scientist's advantage because this allowed them to avoid cross-examination, and they could carefully frame their case instead of attempting to extemporaneously stumble through it on the stand. Milliner gets at the heart of what the Scopes monkey trial case was essentially about in chapter 2—racism. The racist quotes in the biology text used by the school in the Scopes Trial case were clear and damning and would later be used by the Ku Klux Klan to support their unholy racist cause for decades.<sup>3</sup>

Typical of reviews is science writer Debora Mackenzie. In her review of the Scopes trial she makes no mention of the false arguments, and implies that the anti-evolutionists were ignorant, backward folks who had the audacity to oppose science fact.<sup>4</sup> As Milliner documents, not only in the Scopes Trial but also in the other trial he covers, the Dover Intelligent Design Trial (*Kitzmiller vs Dover Area School District*, 2005), evolution blocks reason and the progress of knowledge. Fortunately, the creation worldview



moves forward in spite of the Darwinian impediments.

Milliner shows that every creation–evolution court case that has followed the Scopes trial, including the Dover trial, has followed the pattern set by the Scopes trial. This has produced the same or similar results, both in outcome and intent, even ignoring the problem of erroneous support for evolution.

One point Milliner documents is that a bench trial is no place to rule on evidence for evolution or creation. Most of the scientific arguments are far too complex for a layman such as John Edward Jones III, the judge in the *Kitzmiller vs Dover* Intelligent Design (ID) case. Another problem is the commonality of bias. Judge Jones was openly biased against creationism, even admitting that “This is a case that involved folks who really wore religion on their sleeve. And ... to my mind, that fired me up even more [against the ID view]” (p. 2). An example of the complexity is evolutionists using their claim that two of the middle ear ossicles (of the malleus, incus, and stapes) evolved from the jaw. To do this the evolutionists showed a set of artist drawings that appeared to show this transition. The pictures greatly impressed the judge, even though the

illustrations were based on conjecture taken from just-so stories, not direct evidence. None of the ID supporters involved in the case gave an effective response to this claim, thus the judge accepted this erroneous theory as valid.<sup>5</sup> Nor was the problem of animal jaws changing into two of the ear bones challenged in court. A trial could be held on the ear bone evolution theory alone.

### Intelligent Design confused with creation and religion

The Dover case was covered in detail, noting that one of the evolutionists' main arguments was that creationists wanted to redefine science by allowing supernaturalism into their discussions. Science, former young-earth creationist Brian Alters<sup>6</sup> of McGill University stresses, is about what we can observe, ignoring the fact that the strict empirical method of what we can observe has proven Darwinism wrong by true science (pp. 54, 106, 113).

Typical of the comments plaintiff Tammy Kitzmiller made, when asked if "you feel you've been harmed by the action of the Dover" School Board was her response, "Absolutely. I feel that they have brought a religious idea into the classroom, and I object to that." Of course, religious ideas are regularly brought into the classroom, often indirectly, and sometimes openly. Instruction is not the concern of ID supporters, evolutionary indoctrination is. ID concepts, such as *complex*

*specified information* and *irreducible complexity* should have been mentioned to Tammy Kitzmiller, followed by asking her if *these* ideas, as well as similar ID concepts, were religious. As Milliner notes, those objecting to a religious idea being taught in a public classroom do not typically object to anti-religious information being taught in the public classroom (pp. 67–68). The concern mentioned by Milliner has given rise to the term *snowflake students*, persons censoring information because such students are overly emotional, easily offended, and unable to deal with opposing opinions.

Another example along the same line was the testimony of Aralene 'Barrie' Callahan, who testified, in the Dover trial, that

"Intelligent design is clearly religious. It's not my religion. I am very upset about the idea of a public school trying to influence my daughter's religious beliefs. And that probably is the most harmful."

To this response Milliner comments,

"How does she think the Christian mother who believes in creation feels when the public school tries to undo her daughter's religious beliefs who also believes in creation?" (p. 68)

As Milliner shows, the schools in America and other countries deliberately and openly indoctrinate students into a materialistic worldview and have no pretence of objective education by doing so except calling scientific critiques

against Darwinism 'religion' and scientific support in *favour* of Darwinism 'science', even if the support is erroneous.

The Dover case was essentially about placing a book titled *Pandas and People*<sup>7</sup> in the school library so students could read it if they chose (p. 55). It was not about teaching creation or ID in a science classroom, but rather of allowing students to read the other side. The authors, Percival Davis and Dean H. Kenyon, have impeccable credentials and are both very successful authors and textbook writers.<sup>8</sup> The hatred against *Pandas and People* is openly expressed on Amazon, with 60% giving the book one-star reviews. The reviews are replete with sarcasm and name-calling, showing that the clear majority of reviewers have not read the book.

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Figure 1. Clarence Darrow and William Jennings Bryan at the 'monkey trial' in Dayton, Tenn. in 1925



# Without God the universal cart must come before the cosmic horse

***The Demon in the Machine: How hidden webs of information are solving the mystery of life***

Paul Davies

Penguin Books Ltd., Kindle Edition, 2019

Alex Williams

Multi-award-winning physicist and science writer Paul Davies is currently Regents Professor at Arizona State University and Director of their *BEYOND: Center for Fundamental Concepts in Science*. His awards include the Templeton Prize (1995), the Kelvin Medal (2001), the Faraday Prize (2002), the Order of Australia (2007), and the Klumpke-Roberts Award (2011). His research interests include cosmology, quantum field theory, biology, and astrobiology, and he is chairman of the *SETI: Post-Detection Science and Technology Taskgroup* of the International Academy of Astronautics. He also serves on the Advisory Council of *METI (Messaging Extraterrestrial Intelligence)* and is an adviser to the *Microbes Mind Forum*.<sup>1</sup>

In his *Preface* Davies begins with the question ‘What is Life?’ following Nobel Prize winning quantum physicist Erwin Schrödinger’s 1944 book of the same name:

“I’m not a biologist, I’m a physicist and cosmologist, so my approach to tackling big questions is to dodge most of the technicalities and home in on the basic principles. ... The huge gulf that separates physics and biology ... is unbridgeable without

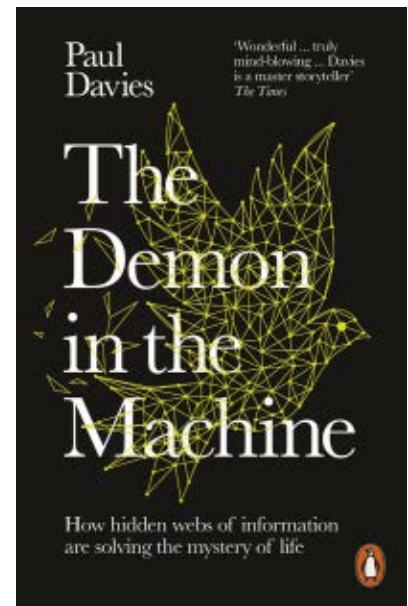
fundamentally new concepts. Living organisms have goals and purposes—the product of billions of years of evolution—whereas atoms and molecules just blindly follow physical laws. Yet somehow the one has to come out of the other” (pp. 1–2, all page numbers refer to Kindle edition).

And what are these “fundamentally new concepts?”

“The unifying concept that underlies this transformation is *information*, not in its prosaic everyday sense but *as an abstract quantity which, like energy, has the ability to animate matter. Patterns of information flow can literally take on a life of their own, surging through cells, swirling around brains* and networking across ecosystems and societies, displaying their own systematic dynamics. It is from this rich and complex ferment of information that *the concept of agency* emerges, with its links to consciousness, free will and other vexing puzzles. It is here, in the way living systems arrange information into organized patterns, that the distinctive order of life emerges from the chaos of the molecular realm [emphases added]” (p. 2).

The book is a good read—telling us about the latest research into the wonders of life—but by the end, all he has to offer is what he says here, that ‘somehow’ disembodied ‘surging’ and ‘swirling’ of information flow patterns becomes the ‘agency’ which brings chemicals to life and brains to consciousness (see figure 1).

For a scholar of Davies’ stature, it is a rather dismal ending to a stellar career.



## Cognitive dissonance

As a self-styled ‘astrobiologist’ (they are all self-styled as they have no subject matter to justify that appellation) perhaps Davies has become so used to living with cognitive dissonance that he simply forgot that information flow patterns—even if they can “literally take on a life of their own”—still require the *hardware* of life to *flow through*. Ignoring the hardware of life (the intricate and irreducibly complex molecular structures in cells) is an egregious error of “basic principles”. It is not only Davies who has made this error, but so too have the many colleagues and reviewers whom he lists on two-and-a-half pages as having helped him review the book!

It is a fundamental characteristic of many complex systems that the whole can become more than the sum of its parts. It is especially true of living organisms, but it is also true of many man-made machines. A classic example is the aeroplane—which is made of parts that cannot fly but when assembled and operated in the correct manner *can* fly. Indeed, that is why we create machines—because the package-as-a-whole can do things that the separate parts cannot. And it is crucially true of living cells or they

would not survive! Life can exist (and persist) only when all parts of cells are present and functional to maintain and repair themselves and endure through procreation. But whatever ‘the whole’ can achieve above and beyond what the parts cannot, that special achievement crucially depends upon the parts and *cannot* exist without them (or at least a functional subset of them).

In his haste to solve the problem of the origin of life and the origin of consciousness Davies has ‘put the cart before the horse’. Information can indeed “surge” and “swirl” through living systems but *only* because they have been designed, constructed, and operated in such a way that enables and uses such information flows. Without the intricate molecular *structures* that make up living systems there would be no *function* which could involve and utilize information flows!

### What is life?

Having put the cart before the horse, Davies nosedives into an entirely inadequate definition of life (p. 24):

“Life = Matter + Information”

He expands upon the definition by highlighting reproduction as the crucial point:

“The essence of biological reproduction, then, is the replication of *heritable information* [emphasis in original]” (p. 24).

This is a standard neo-Darwinian error—viewing heredity as genetic rather than cellular<sup>2</sup>—so we cannot blame Davies for it. However, its erroneous corollary (that evolution is open-ended) is peppered in its consequences throughout the book.

If, as Davies claims, information flow was an *agent* in the origin of life then it must have existed prior to life’s origin. This is another fundamental error in “basic principles”. But, as a physicist, he would have no problem with information existing before life because he knows that he can conjure up any amount of physical (statistical) information from any given mucky

mess of chemicals because it can be mucked about with in infinitely many different ways. That is how physicists calculate the information content of any system—by working out how many different configurations of particles it can be arranged into. All you then have to do is suppose that just one of those ways happened to form a living cell.

But the information that drives and maintains living organisms is far more sophisticated, precise, and durable than that. Life uses *coded* information—a fact that Davies acknowledges but is completely unable to derive from his statistical understanding based in physics. As a result, in his subsequent discussions of life and information, he is doing nothing more than ‘driving blind.’

### Life is ‘demonic’

The ‘demon’ in the book’s title is, of course, Maxwell’s demon. Imagine a sealed box containing gas molecules at equilibrium, having a wall dividing it into two halves and a sliding door in the wall allowing single gas molecules to pass freely, one at a time, between the two halves. Now imagine a tiny ‘demon’ standing by the door ready to open and shut it at will. If the demon chooses to open the door when a faster-than-average gas molecule approaches from one direction, and closes it when slower-than-average molecules approach, and *vice versa* with molecules approaching from the other side, then after some time he could violate the second law of thermodynamics and turn a box of gas at equilibrium temperature into a box with just hot molecules in one end and cold molecules in the other end. That ‘demon’ if it ever existed would be a Maxwell demon!

Note, crucially, that Maxwell demons are *intelligent agents*—a point that Davies must deliberately ignore to justifiably reject an intelligent designer of life.<sup>3</sup>

Lo and behold, Davies reveals that life runs on Maxwell demons!

Yes, the machinery of life ‘steals’ energy from the random jiggling (called ‘thermal energy’) of the atoms and molecules in all its parts in much the same way that an electric bicycle or a hybrid gasoline/electric car draws energy from its environment to supplement its primary power source (a battery).<sup>4</sup>

Having established this fact, Davies then highlights the role of information in life and evolution:

“Evolution operates on biological software just as it does on hardware; we don’t readily notice it because information is invisible. Nor do we notice the minuscule demons that shunt and process all this information, but their near-thermodynamic perfection is a result of billions of years of evolutionary refinement” (p. 109).

Here we see another fundamental error of “basic principles”. As a Darwinist, Davies must subscribe to the ‘slow-and-gradual, simple-to-complex’ model for the origin of life, yet here he admits that it runs on mechanisms that are thermodynamically “near perfect”. In chapter 5 Davies will tell us that life’s ‘demons’ work by drawing on the power of quantum mechanics, but to achieve this they must act extremely quickly and within “stringent design requirements” or they will be overwhelmed by thermal noise. Correspondingly, first life must have also been thermodynamically “near perfect” or it would not have survived, so the supposed “billions of years of evolutionary refinement” had nothing at all to do with it!

To explain the information connection, Davies draws an analogy with computers. He begins with a history of computing, the development of Shannon’s statistical theory of information, its relationship to entropy, attempts to build a Maxwell demon machine, and why computers generate heat. It turns out that Maxwell’s demon doesn’t violate the second law of thermodynamics because the information-processing



required—when repeated over and over again—uses energy and generates waste heat so that overall entropy is increased.

At this point Davies nails both his feet firmly to the floor as he describes the work of Rolf Landauer who,

“... calculated the minimum amount of entropy needed to erase one bit of information, a result now known as the Landauer limit. ... By demonstrating a link between logical operations and heat generation, Landauer found a deep connection between physics and information, not in the ... abstract ... sense ... but in the very specific (that is, dollar-related) sense in which it is understood in today’s computing industry. From Landauer on, information ceased to be a vaguely mystical quantity and became firmly anchored in matter” (p. 46).

By jumping onto Landauer’s work as evidence that information is “firmly anchored in matter” Davies gives himself an excuse to ignore the “vaguely mystical” multiple dimensions of coded information that lie beyond its statistical properties (i.e. semantics, syntax, pragmatics, and apobetics).<sup>5</sup> He refers back to Landauer’s work later when driving home his message about human consciousness:

“... we cannot disconnect mind from matter. As Rolf Landauer taught us, ‘information is physical’, so minds must perforce also be tied to the material goings-on in the brain” (p. 192).

His commitment to materialism is absolute.

### The logic of life

Davies begins chapter 3 as follows: “The story of life is really two narratives tightly interwoven. One concerns complex chemistry ... . The other is about information ...” (p. 67).

Another fundamental flaw in “basic principles”! The “complex chemistry” (a huge challenge to explain

in its own right) must be carried out within an intricately structured system of compartments because many of them are incompatible (e.g. oxidation and reduction) and most of them require single-molecule precision in their reaction sequences. Even the tiniest bacterium—which has no internal ‘walls’—still contains molecular structures which constrain and control the complex chemistry. The *structure* of life is therefore an irreducible foundation for the *function* of life,<sup>6</sup> but Davies entirely ignores it. Despite this, in a long exposition of mathematical logic, he does come to a useful insight:

“Life’s ability to construct an internal representation of the world and itself—to act as an agent, manipulate its environment and harness energy—reflects its foundation in the rules of logic” (p. 72).

And as one of several examples, he commendably cites the award-winning work of Eric Davidson in painstakingly unravelling the Boolean signalling networks that control the early stages of embryo development in the purple sea urchin (p. 106).



**Figure 1.** Jupiter’s Great Red Spot is Paul Davies’ ‘favourite example’ of spontaneous structure formation in non-equilibrium systems, which he offers to show that similar phenomena could be precursors to life. But this is a ‘tornado in a junk yard’ compared to the minuscule mechanisms in photosynthesis which can take single photons of light and turn them into food using quantum weirdness (at ambient temperature) boosted by thermal noise (using Maxwell demons).

### Quantum demons

In chapter 5 Davies introduces quantum mechanics and demonstrates from several examples that life uses quantum ‘spookiness’ to achieve things that would otherwise be impossible. The challenge is that quantum effects occur on such a tiny scale that they are easily overwhelmed by the thermal noise that constantly assails all parts of a cell at ambient temperatures. That is why quantum physics experiments are usually carried out at exceedingly low temperatures where interference from thermal noise can be reduced to almost zero.

The key to life’s success in garnering energy from the quantum realm at ambient temperatures is to do it extremely quickly before thermal noise destroys the ‘magic moment’. In fact, life goes one better and ratchets thermal noise into the quantum transaction to make it go even faster and thus even more efficiently! However, to achieve such marvels of molecular engineering:

“Stringent design requirements must be met to transport charges rapidly and efficiently along specific pathways and prevent the off-path diffusion ... and the disruption of energy flow” (p. 150).

How was this achieved? It was, of course, “honed by evolution” (p. 150). But this argument is self-refuting because he just told us that life doesn’t work (so evolution doesn’t happen) if its mechanisms are either slow or sloppy!

### Almost a miracle

In chapter 6, Davies addresses what he sees as his central challenge:

“In his Dublin lectures Schrödinger identified life’s ability to buck the trend of the second law of thermodynamics as a defining quality. ... By coupling patterns of information to patterns of chemical reactions, using demons to achieve a very high degree of thermodynamic efficiency, life conjures coherence

and organization from molecular chaos” (p.166).

How does life do this?

“Chemistry alone, however complex, can never produce the genetic code or contextual instructions. Asking chemistry to explain coded information is like expecting computer hardware to write its own software” (p. 167).

What then?

“What is needed to fully explain life’s origin is ... the organizational principles of information flow and storage and the manner in which it couples to chemical networks, defined broadly enough to encompass both the living and non-living realms. And the overriding question is this: can such principles be derived from known physics or do they require something fundamentally new (p. 167)?”

Davies rules out probability as an explanation:

“You cannot determine the probability of an unknown process! We cannot put any level of confidence—none at all—on whether a search for life beyond Earth will prove successful (p. 177).”

He then considers experimental attempts to create artificial life and what the conditions might be for a successful outcome. He rejects an intelligent designer, but he comes up with a commendable formula:

“What would swing the debate is if, by synthesizing life many times and in many different ways, scientists uncovered certain common principles which could then be applied to real-world conditions” (p. 179).

This makes sense. If these conditions were ever met, then there would be a case for estimating the probability of life occurring elsewhere in the universe. But, of course, it will never happen.<sup>7,8</sup>

### The ghost in the machine

In his seventh and final chapter Davies considers the enigma of consciousness. He gives an instructive

outline of contemporary thinking based on research outcomes, including theories that include quantum mechanics (e.g. the Penrose–Hameroff theory, which incorporates the effects of anaesthesia [unconsciousness], p. 206). However, he ends up despairing that the question may never be answered.

### Epilogue

In the Epilogue Davies finally shows his cards.

“While it is the case that biological information is instantiated in matter, it is not inherent in matter. ... it is impossible to derive the laws of information from the known laws of physics. To properly incorporate living matter into physics requires new physics. ... nothing less than a revision of the nature of physical law itself (pp. 209–210).

Since “What a system does depends on how a system is”, Davies argues that we require a new set of self-referencing state-dependent laws (of physics) that exert top-down system-level causation (p. 212). I don’t think he actually knows what he is talking about here because this description fits an intelligent design scenario. However, he disdainfully rejects a creator God because:

“It would imply a type of cosmic magician who sporadically intervenes, moving molecules around from time to time but mostly leaving them to obey fixed laws” (pp. 216–217).

His conclusion:

“These speculative notions are very far from a miracle-working deity who conjures life into being from dust. But if the emergence of life, and perhaps mind, are etched into the underlying lawfulness of nature, it would bestow upon our existence as living, thinking beings a type of cosmic-level meaning. It would be a universe in which we can truly feel at home” (p. 217).

### Conclusion

Although this readable book reports a great deal of important progress in our understanding of life and consciousness, its conclusions are unavoidably silly. Davies does not understand biology well enough, nor does he understand biological information well enough, to do justice to his subject matter. The “Demon” in the title of the book is real (Maxwell’s Demon), the “Machine” is real (the awesome molecular mechanisms that use Maxwell Demons), but disembodied “information flows” are certainly *not* “solving the mystery of life.”

Biological errors<sup>9</sup> (plus others noted at [Amazon.com](https://www.amazon.com)) further reduce the credibility of the book and its conclusions. Astrobiologists should get their facts straight about Earth life before they presume to speak about alien life.

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4. An electric bicycle uses pedal power and downhill running to recharge its battery; a hybrid car uses deceleration and downhill running to recharge its battery.
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9. E.g. “human DNA contains about 1 billion bases” (p. 38) when it is more like 3 billion; “the human genome codes for about 20,000 proteins” [i.e. assuming ‘one gene = one protein’] when the number is more like 80,000 to 400,000 according to the *Human Proteome Project*; “entomologists” instead of “entomologists” (p. 102); “When an embryo develops from a fertilized egg, the original single cell (zygote) starts out with almost all its genes switched on (p. 105)” when in fact the opposite is true.



# New book offers needed correction to Christian apologists

## *Myths and Mistakes in New Testament Textual Criticism*

Elijah Hixson and Peter J. Gurry (Eds.)

IVP Academic, Downers Grove, IL, 2019

Lita Cosner

Biblical creationists are no strangers to bad arguments against Christianity. We are also well aware of bad defences of Christianity from compromised positions. But there are also times when we ourselves need correcting, and often it is individuals with specialized knowledge who point out bad or outdated arguments we shouldn't use.<sup>1</sup> It helps when these individuals combine their zeal for accuracy with a love for God's Word, because then we know they are trying to build something better, not to tear down and destroy what is already there. The contributors to *Myths and Mistakes in New Testament Criticism* do a service to all Christian apologists by pointing out some crucial areas where our arguments about the New Testament (NT) manuscripts need to be revised. Their arguments are based on the best evidence currently available and serve as both a warning and an encouragement to the believer.

### Autographs

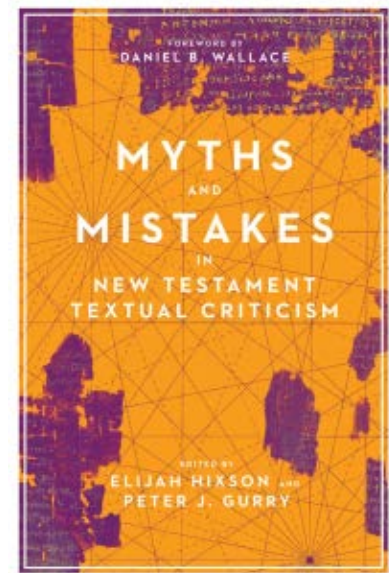
The Chicago Statement of Inerrancy<sup>2</sup> states that the 'autographs' of Scripture are inerrant, but what exactly is an autograph?<sup>3</sup> To answer that, we have to understand what publication of a document in that era entailed. There would sometimes be multiple drafts or early

copies that would precede the 'final' product. This would then be released for circulation and further copying. Also, "it was often a community effort that involved some of the author's closest associates" (p. 35). Furthermore, it is also possible that the author produced multiple 'autographs' of the document to circulate.

Some apologists claim that the autographs could have survived for a very long time and thus stabilized the textual tradition. However, we know that most of the early NT documents were written on papyrus, which only survived well in hot, dry climates like Egypt, and survived poorly in places like Rome that were more humid. And written documents were also often destroyed in fires or deliberately ruined during times of persecution. Furthermore, it seems that it was the *message* of the biblical documents, and not the manuscripts themselves, that were seen as valuable, so early Christians did not necessarily take care to preserve older manuscripts when a good newer copy had been produced. Also, an original copy can only exist in one place. It cannot be easily compared to all the circulating copies of that document. Therefore, the authors state, "It is unlikely that the New Testament autographs still existed and influenced the text by the time of our earliest copies. Even if they did, this alone would not guarantee that the existing manuscripts are reliable" (p. 47). There are other good arguments for the reliability of the manuscripts that we have; this simply happens not to be one of them.

### Manuscript numbers

One of the staple arguments for the reliability of the NT text is how many

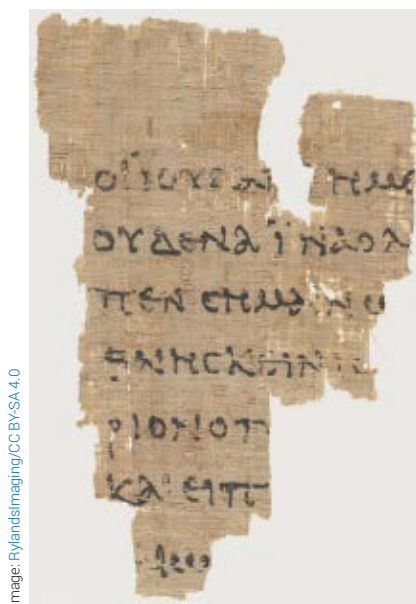


copies of the New Testament documents were preserved—far more than for any other work of antiquity. While this is valid, many people have failed to keep up with the latest research, or inadvertently don't compare manuscript numbers fairly. While the overall argument can still be used, *Myth and Mistakes in New Testament Textual Criticism* gives some needed correction.

Many commentators, from evangelical apologists to Bart Ehrman, have claimed there are far fewer ancient manuscripts of non-biblical works than there actually are. This is because the numbers were once accurate but are now outdated. Just as more biblical manuscripts have been discovered, more manuscripts of other ancient works have also been uncovered.

Furthermore, it is difficult to count precisely how many biblical manuscripts we have. This is because some fragments that were originally catalogued as separate documents are part of the same manuscript so should be counted together. Others were catalogued once, lost, then rediscovered and catalogued again. Some manuscripts have been destroyed and thus can no longer be counted in the total.

*Myths and Mistakes* points out an inconsistency in how biblical manuscript numbers are compared with other



**Figure 1.** P52 is dated paleographically to AD 100–200

ancient works. Often, only the ‘good’ or ‘significant’ manuscripts of the non-biblical works are counted, but every scrap containing only a few words or clearly derivative biblical manuscript is counted toward the total of biblical manuscripts.

Because it is hard to count manuscripts precisely and the numbers are always shifting as new research is conducted, we should use non-specific numbers and consult recent scholarship for the best possible information.

### How early are the manuscripts?

Several years ago biblical scholar Daniel Wallace mentioned a first-century manuscript of Mark that had yet to be revealed to the public in a debate with Bart Ehrman.<sup>4</sup> However, when it was finally published, the truth was far less spectacular—it was not a particularly early copy.

We believe that the New Testament was completed before the end of the first century, and early copies provide both a *terminus ad quem* for its composition and evidence for the specific wording of the original text. But most manuscripts can only be dated

by paleography—analysis of the handwriting. This can only give us a range within a century or so. This means, for instance, the John manuscript P52 (figure 1) was written somewhere between AD 100–200, not necessarily AD 125, as is often claimed. It is still an early manuscript fragment, but we cannot be that specific.

Even if some of the manuscripts are not as early as previously claimed, the real evidence for the trustworthiness of the text is how little the text has changed over time. We can see this by comparing a new recreation of the Bible using text-critical techniques (the *Editio Critico Maior*) to the later Byzantine manuscripts. The text of Acts and the general epistles agree 94% of the time, and the Gospels agree at least 86% of the time (p. 116). In fact, “the core tradition remains remarkably stable over time, in that the difference between the two texts usually thought to be most polarized is actually fairly small” (p. 116).

### Were the early copyists professional, amateur, or something else?

It is often claimed that the early copyists of the New Testament were amateurs, and this resulted in more errors than would have been expected otherwise. Some apologists have claimed the opposite—that the early copyists were highly literate and made few mistakes or intentional changes. In reality, the manuscripts of the New Testament reflect “a wide range or scribal skills and abilities among the early manuscripts, but a majority appear to be competent transcribers” (p. 151).

Additionally, manuscripts were corrected, sometimes by the original copyist and often by later hands. The corrections “show that scribes strove to improve and revise their work” (p. 170).

### Most variants are not significant

There are no two identical hand-copied manuscripts of any biblical text.

However, while there are more variants than words in the New Testament, the vast majority of those have to do with spelling or word order. Only a small number of variants are both *viable* (i.e. they could be the original reading) and *meaningful* (they make a difference to the reading of the text). While there are small places where we cannot be 100% certain of the original reading, these instances do not affect doctrine.

One of the most interesting chapters in the book was a comprehensive overview of the manuscript tradition for Philemon which highlights the number of variants that exist that are not discussed in most exegetical analyses because they are certainly not original. However, “textual variations that aren’t original can still help us to understand how the text was understood in some settings” (p. 190).

### How much did early Christians change the Scriptures? And how much of the Bible did their quotations preserve?

A common skeptical argument claims that theologically motivated church authorities changed the Scriptures to remove beliefs they deemed heretical. We know that, at least in some cases, there are theologically motivated edits to particular manuscripts. These can be identified by looking at an entire manuscript as a whole. The advantage to having so many manuscripts is that these theologically motivated edits never replaced the original readings.

Some apologists make the claim that even if we had no New Testament manuscripts we could reconstruct the entire New Testament (minus 11 verses) from patristic sources. However, this is false. Even if it were true, it would be circular because you would still need the New Testament to be able to distinguish a genuine quote from an allusion or paraphrase. And you would not be able to order the quotations within a specific book or even necessarily know which quotations belong in which book. So, on the one hand, yes, the New Testament



is extensively quoted in early Christian writings. But, on the other hand, this does not mean we could recreate it. However, the early commentaries give us an excellent additional source of validation for the New Testament text. We know what it says because we have so many copies, so many early copies, so many early quotations, and so many early translations into other languages.

### Becoming comfortable with some degree of uncertainty

We like to make statements with as much certainty as possible. After all, we are dealing with a book that is inerrant—we are *certain* that it is true. However, there is a difference between the amount of certainty we can claim for the doctrines of Christianity and the certainty we can claim for particular arguments in the defence of Scripture. No one should lose their faith because we need to claim a wider date range for P52, or because we have slightly more manuscripts of Homer's Iliad and slightly fewer NT manuscripts than was previously claimed.

*Myths and Mistakes in New Testament Criticism* provides an important service in correcting some overly simplistic, outdated, and flawed arguments. It also provides improved arguments for the reliability of the New Testament manuscript tradition. It assumes some knowledge of technical terms but is written in an engaging style that should be accessible for the interested layperson. Thus, this book is highly recommended for the student of Scripture.

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## Dealing the special creation trump card to the Catholic church's evolution-stacked deck

### *The Evolution of Catholic Unbelief*

Thomas L. McFadden

Institute for Science and Catholicism, 2019

John Woodmorappe

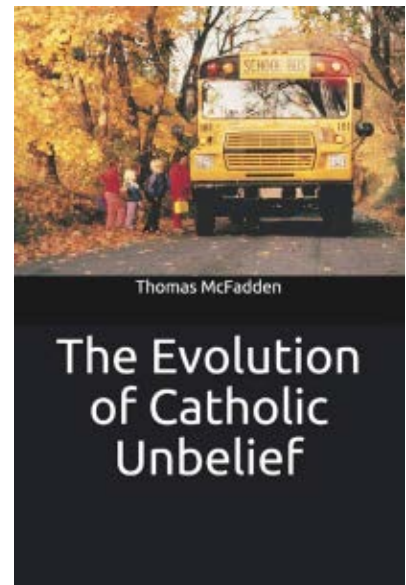
The book's author is an engineer. He is concerned about Catholic youth rejecting the Faith, and doing so out of deference to evolution, which has long permeated the Church. While much of his material imitates conservative Protestant modes of thinking, some of it is Catholic-specific, and he shows some unique insights into the creation–evolution issues. Because most readers of this review are not Catholic, I tailor my review to de-emphasize Catholic-specific issues.

Some readers may not be comfortable with the author's style. He uses a free-flowing narrative that injects references within the text itself and which mixes literary sources with references to websites and YouTube presentations. But his message does get through loud and clear.

Author McFadden includes a detailed list of creationist and ID organizations and their websites. One seldom-noted organization is a Catholic one, the Kolbe Center for the Study of Creation ([kolbecenter.org](http://kolbecenter.org)).

### Statement of the problem: the fruits of evolution

The author cites statistics that show that half the American Catholic



children baptized and confirmed in the last 30 years are now ex-Catholics or religiously unaffiliated. Part of this resulted from what McFadden calls the ‘dumbing down of the faith’. McFadden rejects the common media spin that the falling away is governed by disagreement with the Church on such ‘hot button’ issues as contraception, same-sex marriage, or clergy sex-abuse. In fact, he cites many ex-Catholics pointing to the “disconnect between religion and science” as the reason for their unbelief.

The foregoing is part of a deeper trend. The author writes:

“More than half of U.S. adults view science and faith as being ‘often in conflict.’ Given the weight and prestige of science in our culture, that puts faith in a corner. Simple

affirmations in favor of religious tradition or naïve apologetic approaches won't suffice—not least with young people as they encounter a range of challenging viewpoints” (p. 67).

McFadden elaborates on the bitter fruits of evolution. He comments:

“Evolutionary cosmology and evolutionary biology which are the materialist scientific consensus are taught as if they were proven facts to children from their earliest school days. The Church, which has the truth about our origins, has ceded the education of its youth on these matters to the secular culture to provide explanations for which no God was necessary” (p. 3).

He adds:

“At some point, teenagers recognize that the naturalistic evolutionary model of origins and the supernatural, fiat creation model described in the Bible, which they have heard read at Mass even if they never opened a Bible, can't both be true. They experience cognitive dissonance, and, to relieve the conflict, they must alter their beliefs in one direction or the other. According to the social researchers, too many teens resolve the disconnect between religion and science in favor of science” (p. 6).

### **Evolution unfairly rides the coat tails of scientific prestige**

McFadden elaborates on how youth tend to equate the presumed factuality of evolution with the actual factuality of experimental science:

“After all, ‘science’ delivers the goods such as the machines and gadgets that enrich our lives. The fact is that's engineering based on operational/empirical science; the ‘science’ of cosmic and biological evolution is speculation based on inferences from historical data. The mechanism by which it happened

remains unknown and bound in conundrums. It's tooth fairy science . . . . Most Catholic adults (including clergy) are not informed on these matters so they can't help the kids discriminate between ‘faux science’ and real science” (pp. 6–7).

### **From the beginning, evolution rested on speculation, not evidence**

Author McFadden discusses Darwin's *Origin of Species*:

“However, far from being a definitive work, the *Origin* is saturated with conjecture. In the final 1876 printing of the 1872 sixth edition, Darwin employed the word ‘may’ 642 times, ‘if’ 493 times, ‘might’ 203 times, ‘probable’ or ‘probably’ 182 times, ‘tend’ or ‘tendency’ 153 times, ‘suppose(d)’ 141 times, ‘perhaps’ 63 times, ‘no doubt’ 58 times, ‘I believe’ occurs 58 times, and so on. Yet Darwin's disciples hold a belief in the fact of evolution with a zeal that only their non-theistic religion can inspire” (p. 86).

### **The church was intimidated, almost from the beginning, into going lockstep with evolution**

Shortly after the *Origin of Species* came out, a group of German bishops condemned it. McFadden adds that “There was in fact a consistent, if relatively quiet, rejection of human evolution on the part of the See of Peter throughout the last three decades of the nineteenth century” (p. 50). The Church generally avoided the issue, having been ‘burned’ by the experience with Galileo centuries earlier.

In 1894, Fr Leroy wrote a book promoting a ‘Christian’ evolution. There was some controversy, but Fr Leroy's book was not placed on the *Index of Forbidden Books*. Fr Luigi Tripepi criticized the book. He appealed to Church tradition in upholding the

factuality and literalness of Genesis 1. He objected to the speculative and *ad hoc* nature of various proposed ‘reconciliations’ involving theistic evolution, and, anticipating modern creationists, raised numerous scientific objections to evolution.

### **A spirit of appeasement**

Finally, Fr Tripepi identified the *real* cause of the Church seeking a ‘reconciliation’ with evolution. McFadden writes:

“He [Tripepi] denounces the cowardice of too many contemporary Catholic scholars, who, by their excessive fear of what ‘science’ has to say, manifest nothing but the weakness of their own faith” (p. 48).

Powerful words! And so true.

### **The floodgates of compromise are open**

One compromise leads to another. Jesuit priests George Tyrrel (1861–1909) and Alfred Loisy (1857–1940) became so enamoured with evolution that they rejected supernatural revelation entirely and ended up leaving the priesthood and the Church. (According to other sources, they had been excommunicated by the Church.) In either case, they had, thanks to evolution, gone off the humanist deep end. And who could forget Fr Pierre Teilhard de Chardin, the famous renegade priest who essentially redefined Christianity in terms of evolution? In recent times, Fr. Bruce Vawter, who testified for the successful evolution-monopoly side at the Arkansas Trial in 1981, was effectively a disciple of Rudolf Bultmann, a prominent theologian who “demythologized” the Bible.

The foregoing can be generalized. For many decades, Catholic theology has come to be dominated by the modernism of Bultmann, who not only adhered to evolution but systematically



denied everything miraculous in the Bible. All the biblical events were arbitrarily redefined and trivialized. Thus, for example, Jesus' feeding of the 5,000 became nothing more than the masses of people getting persuaded to share their food with each other! The Resurrection of Jesus Christ was nothing more than an emotional 'encounter' that Christ's disciples had with His memory after the Crucifixion.

### Avoiding the conflict entirely

Nowadays, more often than not, the Church buries its head in the sand. By not discussing the issue of special creation, the Church sends an unspoken message that the Bible is mistaken on this matter. McFadden comments:

"Cardinal Ratzinger, who became Pope Benedict XVI, published in 1995 a book called *In the Beginning* ... In that book's preface the Cardinal wrote that: '... the creation account is noticeably and completely absent from catechesis, preaching, and even theology. The creation narratives go unmentioned; it is asking too much to expect anyone to speak of them'" (pp. 8–9).

### The vague character of theistic evolution

When the issue is raised at all, it is always the same. Evolution is never questioned. McFadden realizes the

self-refuting nature of theistic evolution: An inherently unguided process is now supposed to be guided by God. In fact, the only difference between theistic evolution and atheistic evolution is that the former employs theological language, albeit empty theology, to make its case.

The author repeatedly stresses the fact that the commonly voiced "God was behind it" assertions are superficial. He writes:

"It is one of these 'god-of-the-gaps' explanations on which theistic evolutionists rely to keep 'one foot in each camp,' so as to speak. They have no coherent explanation compatible with the theory of evolution. What it really may indicate is the shallowness of their understanding of the implications of a scientific hypothesis they otherwise support as a better explanation of cosmic and biological origins than the Bible. It is very facile for such Catholic evolutionists to pose as 'scientific' and 'orthodox' but a little more difficult for them to expend the mental energy necessary to become coherent in their belief" (pp. 27–28).

### Retaining a 'literal' Adam and Eve in a framework of theistic evolution

Compromising evangelicals that promote theistic evolution typically

dismiss Adam and Eve as real people. In contrast, many Catholic theistic evolutionists allow for a 'real' Adam and Eve. All the animal and human evolution takes place exactly as in the atheistic scenario. However, at some point in human evolution, God steps in and infuses a soul into a hominid male individual and a hominid female individual. These are the 'Adam and Eve' as understood by Catholic theistic evolutionists.

Their 'Adam and Eve' scenario is internally inconsistent. It arbitrarily allows God to perform a miracle within a system that completely excludes the miraculous. It is also anthropocentric and God-restricting. Evolutionary theory is changed in order to make the appearance of humans something special, while strict naturalism is maintained in order to account for the appearance of animals and plants.

The scenario arbitrarily picks and chooses which events are factual and which are not. Thus, 'Adam and Eve' technically existed, but Adam was not made from the ground, and Eve was not taken from Adam's side. Death long pre-existed this 'Adam and Eve'. They had parents.

Absent another *ad hoc* miracle, this 'Adam and Eve' pair can still reproduce with other hominids, so, in no sense are these 'Adam and Eve' the biological parents of us all. It also contradicts Catholic dogma. Note that



Figure 1. A classic painting of creation by Michelangelo

Pope Pius XII, in *Humani Generis*, had taught that all humans are descended from Adam. Without miraculously imposed reproductive isolation, they are not.

Though not mentioned by McFadden, the whole scenario is unrealistic on its face. According to evolution, there is, to begin with, no such thing as a soul. We are nothing more than a bundle of animal drives and reflexes, different in degree but not in essence from all other animals.

Finally, McFadden points out that the entire scenario is completely *ad hoc*. He writes:

“Even supposing for the sake of argument that this hypothesis could be shown not to be intrinsically contrary to revealed truth, it suffers from the fatal defect of being totally gratuitous: that is, there is no positive evidence whatever from either revelation or reason to suggest that it is true. Rather, it seems like a desperate attempt to mix together two radically different world-views that cannot blend in with each other any better than oil and water” (p. 54).

That’s a succinct way to put it. It professes to be both scientific and religious, but it is neither.

### Non-literal Genesis days? The *reductio ad absurdum*

In common with compromising evangelicals, Catholic theistic evolutionists assert that the days in Genesis 1 can be long periods of time, based on the fact that “a day to the Lord is like a thousand years” (e.g. 2 Peter 3:8). McFadden points out that this is a simile. After all, if (A) is *like* (B), this is not the same as saying that (A) *is* (B). Besides, such usage of this verse is self-refuting: 2 Peter 3:8 also says that “a thousand years as one day”. So, instead of supporting the Day–Age theory, it could just as easily argue that the creation took place over a much *shorter* period than six natural

days and could even have happened instantaneously. Such is the *reductio ad absurdum* of making the Bible say anything that one wants it to say.

In fact, according to the author, Thomas Aquinas argued for an instantaneous creation (p. 39; though some say he taught six literal days). Aquinas, according to the author, maintained that Genesis 1 taught six days because the original recipients of the text were “not educated enough” to grasp an instantaneous creation. Now modern compromising evangelicals tell us the exact opposite: They assure us that Genesis 1 says six days, but actually refers to a long period of time, because the original recipients of the text were “not educated enough” to grasp a creation over extended periods of time! That is what happens when one insists that the Bible cannot mean what it says because “ancients were dumb”.

### Genesis 1 is literal

The word *yom* can mean a long period of time. But the context must clearly justify it. McFadden points out that Day–Age theorists commit the fallacy of an unwarranted adoption of an expanded semantic range. Just because a word may mean something in some other context, it does not mean that it does so in Genesis 1.

Whenever the word *yom* is modified by a cardinal number (one ... two ... three) or an ordinal number (first ... second ... third), used a total of 359 times in the Old Testament, it always means a literal day of 24 hours, or refers to the light portion of the day–night cycle. In Genesis 1, there is a cardinal or ordinal number after each *yom*.

McFadden points out that Genesis 1–3 has a narrative structure. It is not figurative or allegorical literature. It has numerous intertextual links with other Old Testament verses, not to mention New Testament ones. The genealogies are another hallmark of historicity.

### Paradoxically, evangelicals are now more ‘Catholic’ than most Roman Catholics.

The author quotes from a December 2013 study, conducted by the Pew Research Center, on Americans. He writes:

“The report said that 68% of white, non-Hispanic Catholics believe that humans evolved from animals over time and just 26% believe that humans existed in present form since the beginning. The only groups with a higher belief in human evolution than white, non-Hispanic Catholics are the unaffiliated (76%) and mainline Protestants (78%). Among white Evangelical Christians, 64% believe that humans were created as they are now, just as the Fathers, Doctors, Councils and Popes have taught” (pp. 7–8).

### Conclusion

The Catholic Church has imbibed the bitter poison of evolution. It has taken over not only science, but also all aspects of Catholic learning. The Church is now in lockstep with evolution, largely out of fear of being ‘unscientific’. Meanwhile, the compromise with evolution does not impress anybody. Young people are leaving the Church in considerable numbers, owing largely to the irreconcilability of evolution and Church doctrines.

Hope for a turnaround is offered by some Catholic creationist organizations. They imitate Protestant creationist organizations and have done some original thinking of their own. More power to them!



# How the Catholic Church sold out to evolution

***Creation, Evolution, and Catholicism:  
a discussion for those who believe***

Thomas L. McFadden

Institute for Science and Catholicism, 2020

John Woodmorappe

In this book, the engineer author surveys the encounter of the Catholic Church with evolution. This book is a sequel to his *The Evolution of Catholic Unbelief* (2019), reviewed also in this journal.<sup>1</sup> Because most readers of this review are not Catholic, I try to focus on matters of broad interest.

The author has an unconventional style of writing. He uses a free-flowing narrative that injects references within the text itself, and which mixes literary sources with references to websites and YouTube presentations. But his message does get through loud and clear.

## Evolution leads to outright atheism

McFadden is especially concerned about Catholic youth rejecting the Faith, and doing so out of deference to evolution, which has long permeated the Church. He experienced this personally:

“Years ago, I became aware of the skepticism among Catholic teens while teaching CCD [Confraternity of Christian Doctrine] when they asked me ‘You don’t really believe in Adam and Eve, do you?’ I learned from them that their unbelief in supernatural doctrines derived from the Bible was because of their belief in evolution. They realized

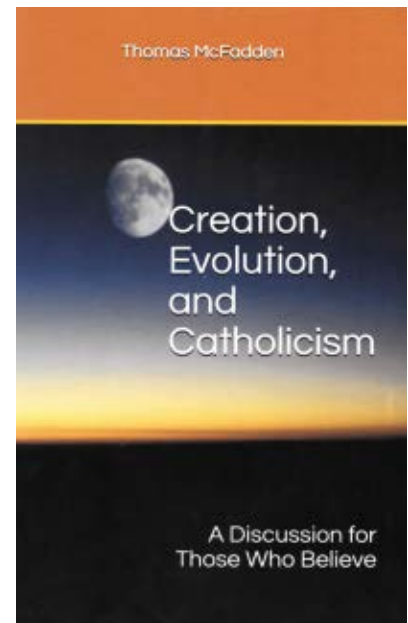
that there was a conflict between the Book of Genesis and the ‘science’ they were taught in school: their school teachers were more effective than their religious educators and had so much more of the students’ time to make their case” (p. 1).

This experience with American youth has parallels with other cultures. In once solidly Catholic Ireland, now only 37.5% of Irish university students believe in God (p. 195). The number in the general population is probably similar, because a referendum to repeal Ireland’s ban on abortion was passed 66.4% to 33.6%. In Australia, less than 50% of Generation Y youth (aka ‘millennials’, born between about 1981 and 1996) indicate a belief in God (pp. 172–173).

## Francisco Ayala and the Spanish experience

This stellar evolutionist (b. 1934) was once a Dominican priest in Spain, but only for one year, in 1961. He became so enamoured of evolution that he came to the USA and studied under Theodosius Dobzhansky (1900–1975). Ayala eventually became president of the American Association for the Advancement of Science and was advisor to the Templeton foundation. McFadden sees Ayala’s experience as a harbinger of what happened to Spain’s once-formidable Catholic faith. Ayala became a bitter opponent of both scientific creation and biblical creation.

McFadden does not mention the fact that Ayala was terminated from his long-term faculty position at the University of California over substantiated allegations of sexual harassment. His



name was stripped from the university buildings named after him.

## Intimidating the church: misusing Galileo and Bruno

Common misconceptions about how the Church handled Galileo and Bruno were and are used to silence any potential criticism of evolution. After all, the Church was wrong to ‘touch’ science once, and had better never try that again. Pope John Paul II actually issued an apology for the Church’s ‘scientific incompetence’ in the Galileo affair. McFadden will have none of it.

He realizes that “The Vatican Congregation involved judged and acted entirely reasonably based on the facts of 1616. In fact, science wasn’t even the primary issue of the Case” (p. 208). He adds:

“Galileo, although he seemed to believe in the heliocentric model, taught the geocentric model at the University of Padua from 1592 to 1604 for fear of being ridiculed. Besides that, the Catholic Church never ‘held’ the geocentric model as a doctrine although it was the

scientific consensus until at least 1687” (p. 244).

That the Church was following the *best science of its time* was thoroughly documented by physicist Christopher Graney.<sup>2</sup>

Giordano Bruno, likewise, was not just some kind of scientific martyr that fell victim to the Church’s resistance to scientific enlightenment. McFadden writes:

“What the anti-Catholic, Darwinist writers ‘forgot’ to mention was that the Dominican priest Bruno was actually convicted as a denier of the Trinity, the divinity of Jesus, Mary’s virginity, transubstantiation, and he was a pantheist. It had nothing to do with science” (p. 244).

Real scientists who supported the geokinetic model, such as Galileo and Kepler, had utter contempt for Bruno. Australian atheistic history writer Tim O’Neill described him as a “mystic” who “scorned empiricism and rejected mathematics as a way of understanding the world”.<sup>3</sup>

### Ernst Haeckel on the church’s sellout to evolution

In Darwin’s time, the Church quietly opposed evolution. By the late 19<sup>th</sup> century, however, and based partly on its memory of getting ‘burned’ by the Galileo affair, it ‘made peace’ with evolution.

Haeckel, a militant atheist, was probably a more capable promoter of evolution than Darwin himself, and is well known for his fake embryo drawings that convinced many of the ‘fact’ of evolution. In his 1906 book, *Last Word on Evolution*, he comments on the Church’s about-face on evolution:

“... the interesting efforts that the Church has lately made to enter into a peaceful compromise with its deadly enemy, Monistic science. It has decided to accept to a certain extent, and to accommodate to its creed (in a distorted and mutilated form) the doctrine of evolution, which it has vehemently opposed

for thirty years. This remarkable change of front on the part of the Church militant seemed to me so interesting and important, and at the same time so misleading and mischievous ... . Our science of evolution won its greatest triumph when, at the beginning of the twentieth century, its most powerful opponents, the Churches, became reconciled to it, and endeavored to bring their dogmas into line with it” (p. 260).

Haeckel’s statements are instructive. One can see from Haeckel’s quoted statements that evolutionists simultaneously praise and despise Christian compromise with evolution. We also see how unilateral appeasement of evolution by Christians leads to demands for more concessions. This is illustrated by Haeckel’s derogatory remarks (‘distorted’, ‘mutilated’, ‘misleading’, and ‘mischievous’). Evidently, leading humanists will not be satisfied with anything less than a complete capitulation to their worldview.

### Evolution drives modernism

Even though the Church hesitantly accepted evolution by the turn of the

20<sup>th</sup> century, it still recognized the toxicity of evolutionary thinking. McFadden comments:

“In 1884 Pope Leo XIII identified the attack on faith caused by naturalism and evolutionism. And in a 1907 encyclical, ‘On the Doctrine of the Modernists’ Pope St. Pius X described how evolution undergirded Modernism which he labeled ‘the synthesis of all heresies’” (p. 15).

Much the same theme is continued in the 1950 encyclical *Humani Generis*. The usually unmentioned context (the early part of the encyclical) partly alludes to modernism as it focuses on bad philosophy spreading through Catholic institutions. It also warns of the dangers of Communism, and how it has used evolution to promote atheism for its own ends.

### *Humani Generis* allows Catholics to skeptically accept some evolution

*Humani Generis* has commonly been misrepresented as a wholesale Catholic endorsement of evolution. It most certainly was not. One can see the caution and doubt toward evolution exhibited by *Humani Generis*, as quoted by McFadden:



**Figure 1.** Adam and Eve have long captured the public imagination. Attempts to combine Adam and Eve with evolution are futile.



“For these reasons the Teaching Authority of the Church does not forbid that, in conformity with the present state of human sciences and sacred theology, research and discussions, on the part of men experienced in both fields, take place with regard to the doctrine of evolution, in as far as it inquires into the origin of the human body as coming from pre-existent and living matter—for the Catholic faith obliges us to hold that souls are immediately created by God. However, this must be done in such a way that *the reasons for both opinions, that is, those favorable and unfavorable to evolution, be weighed and judged with the necessary seriousness, moderation, and measure ...* [emphasis added]” (p. 123).

#### Further unilateral Catholic concessions to evolution

Pope Pius XII made the binding theological statement that all humans are descended from one man—Adam (p. 129) (figure 1). This imposes an arbitrary dualism on the Bible: the Bible is factual about all humans descended from one man, Adam, but is not factual about just about anything else in Genesis 1. The Adam-is-real position also contradicts evolution, in which humans evolved from a population of pre-human hominids, and not from “the first man Adam” (1 Corinthians 15:45).

So-called theistic evolution imposes another artificial dualism on the Bible—that between ‘factual information’ and ‘spiritual information’. Only the latter is inspired and inerrant.

Still another layer of contrived dualism was imposed by the document *Dei Verbum*. It is the dualism between ‘essential spiritual information’ and ‘nonessential spiritual information’, Promulgated by Pope Paul VI in 1965, *Dei Verbum* would have us believe that the Bible is inerrant only in the

spiritual information that specifically pertains to salvation.

The manipulative and self-serving character of *Dei Verbum* was exposed by Father Brian W. Harrison, who declared:

“For when faced with any seemingly erroneous statement of a biblical author, the apologist or Scripture scholar who follows the [proposed interpretation] teaching will inevitably be led to ask the obvious ‘why’ question: ‘Is this statement here *for the sake of our salvation, or not?* And if he can persuade himself that the problematic biblical affirmation is *not* salvific in purpose (as he almost certainly will when it is about history or the physical cosmos), then he will complacently dispense himself from the task of having to defend its truth [italics in original]” (p. 167).

#### Other papal giveaways to evolution

In 1996, Pope John Paul II revisited *Humani Generis*, and raised the profile of evolution. He said that, with the passage of half a century, we now realize that evolution is ‘more than a hypothesis’, and that there is ‘now a significant argument in favor of this theory’ (p. 266). The old tentativeness regarding evolution, in *Humani Generis*, has disappeared.

The current Pope, Francis, has a long history of supporting evolution and other heresies, and this has prompted some traditionalist Catholics to suspect that he is a heretic and false pope. When it comes to evolution, Pope Francis went beyond supporting it. He made some snide remarks about fiat creation—ones that would entirely be expected from an atheist. He said:

“God is not ... a magician, but the Creator who brought everything to life. Evolution in nature is not inconsistent with the notion of creation, because evolution requires

the creation of beings that evolve” (p. 266).

Note the doubletalk. And evolution does not ‘require’ anything. If and when conditions are right, it just (supposedly) happens, independent of the will or guidance of any external agency.

Was God a magician when He raised Lazarus from the dead? Is God a magician, at every Mass, when, according to Catholic belief, the bread and wine become transformed into the very Body and Blood of Jesus Christ? [In fact, ironically, the magical incantation, hocus pocus, is believed to derive from when the priest says *hoc est corpus meum*, which, in Latin, means “This is My Body”.]

#### An excellent riposte to theistic evolution and its censorship and thought control

McFadden cites Thaddeus Kozinski, the former Academic Dean and Associate Professor of Philosophy at Wyoming Catholic College. Kozinski shows how evolution flies in the face of both science and theology:

“I am speaking of the Catholic theistic evolutionists. They overstep *science’s* bounds when they claim that debatable theories, such as the theory of evolution, are ‘facts’—something that Pius XII condemned very unequivocally with regard to evolution in *Humani Generis*. They overstep science’s bounds again when they attempt to render certain non-verified, non-facts, such as common descent from mono-celled organisms, as verified, indisputable facts by recourse to, not actual indisputable evidence, but the social force of the so-called ‘scientific consensus’, that same force that fires and character-assassinates people who publish peer-reviewed scientific articles that conclude to, say, intelligent design of certain processes, and that excludes anyone but committed evolutionists to the Pontifical

Academy of Sciences ... . They overstep *theology's* bounds when they dismiss the very serious challenges, not just to evolutionary theory, but to the very fact of evolution itself, from not only the Catholic Magisterium and Fathers of the Church, but also from the latest scientific evidence, which has, it must be said, proved neither common descent of humans from primitive organisms, nor the generation of all life, in all its glorious complexity and design, from mindless natural selection conserving random genetic variation and mutation [italics in original]" (pp. 136–137).

### Evolution is not the foundation of biological science

It is often argued that all of modern science rests upon the correctness of evolution. This is very far from the truth. McFadden cites the following thoughtful words of Dr Marc Kirschner, the chair of the Department of Systems Biology at Harvard Medical School (the 25 Oct 2005 issue of the *Boston Globe*) as follows:

"In fact, over the last 100 years, almost all of biology has preceded independent of evolution, except evolutionary biology itself. Molecular biology, biochemistry, physiology, have not taken evolution into account at all" (pp. 108–109).

### A change in worldviews: not a change in evidence

McFadden stresses the fact that evolutionary thinking has not taken over the Magisterium, the Pope, or the Vatican congregations. It has taken over the clerical intellectuals. Even long-past Catholic thinkers have now—retroactively—become 'evolutionized'. McFadden cites Fr Chaberek's *Aquinas and Evolution*, in which Chaberek describes how the new evolutionary paradigm 'overlays' previous thinkers:

"As we have noted, it is not the understanding of Aquinas or evolution that has changed over the last century or so. It is rather the change in paradigms—from roughly speaking 'Biblical' or 'creationist' to 'naturalistic' or 'evolutionary'. This change of paradigms explains why a great number of today's Thomists greatly differ from those of a century ago ... we believe that not today's, but the previous Thomists were closer to the truth regarding both—the interpretation of Aquinas's metaphysics and the assessment of the evolutionary theory of origins" (p. 259).

### The remedy for apostasy

Business-as-usual will no longer do. McFadden makes this clear:

"Typically, they say it doesn't matter how everything got here as long as one believes 'God did it'. Nevertheless, the evidence that children are leaving in droves because instruction at school which credits evolution creates a perceived conflict with religion has been 'stacked and catalogued'. Yet priests and parish Directors of Religious Education just keep doing the same things that have failed for the last 50 years. Catholic apologetics needs to embrace the 21<sup>st</sup> century natural science that refutes those bogus 19<sup>th</sup> Century theories instead of 'interpreting' the Bible to fit them. The creation doctrines that the spokesmen for the Church seem to have forgotten or misplaced must be taught again" (p. 18).

More power to him!

### Conclusions

As is the case with many Protestant Churches, the Catholic Church has been attempting, for over a century, to bend Scripture in various creative ways to make it fit evolution. It

has never worked. Late is the hour. With the widespread apostasy from the churches, it is high time that the Church return to an unequivocal and literal acceptance of the Book of Genesis, and teach this without apology.

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# Archaeology's support of the history of the Scriptures

## ***The Case for Biblical Archaeology: Uncovering the historical record of God's Old Testament people***

John D Currid

P and R Publishing, Phillipsburg, NJ, 2020

John G Leslie

The book *The Case for Biblical Archaeology: Uncovering the historical record of God's Old Testament people* is a well-written overview of the study and use of archaeology in the Middle East to better understand historical biblical events. The author is a known archaeologist and Christian teacher/writer.<sup>3</sup> Its focus is on how the Old Testament historical writings and archaeology of the areas of those writings interface. It is composed of three basic sections after an Introduction:

*Part 1: Geography/Topography* covers the basic areas north to south, starting in Galilee in the north, Judean Wilderness, Negev, Coastal Plain, Shephelah, Central Highlands, Jordan Valley, and the Trans-Jordan. It briefly describes the terrain and key archaeology sites in these areas. It contains maps of the major countries in the region.

*Part 2:* A more detailed discussion regarding geographic information as it relates to the archaeology of the region. This includes looking at specific archaeology sites such as Tell Dan (figure 1) and Tel Hazor and others in each of the basic areas. Included are several maps that focus on more local areas and include current political demarcations.

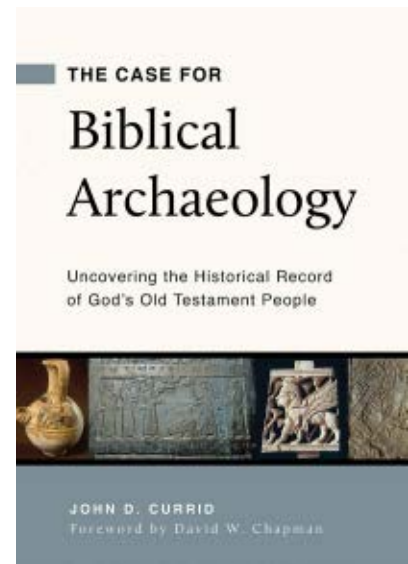
*Part 3:* An overview of the results/interpretation of the results of

archaeology as it relates to the culture of Israel in the Old Testament. Sections include agriculture, water sources, and architecture in the standard Chalcolithic, Early/Middle/Late Bronze Age, and Iron Age divisions. Pottery, use of Hebrew in archaeology (on ostraca, singular ostrakon, = broken piece of pottery), religious practices, and burial practices are discussed. There are frequent references/notations to various books of the Old Testament.

The book is composed of an introduction, 19 chapters divided into the three divisions mentioned above, and some appendices. At the end of each chapter are study questions, references for further study of the subjects of the chapter, and occasionally key terms. There are maps and various photos of key archaeological finds that support the biblical history and archaeology of some of the chapters. Examples include the Rosetta Stone (important in interpreting the Egyptian hieroglyphics), a Lachish ostrakon (documenting the Babylonian invasion of Judea), a Hezekiah royal seal, and many other items. It appears to be designed for a student to use.

## Introduction

Chapter 1 is salient in that it briefly covers an overview of the field of archaeology of the Middle East, biblical tells (mounts where ancient cities were located), the process of excavation, and a brief history of the land from a hunter/gatherer phase until the Babylonian Exile. The author follows a traditional stagewise development of mankind from Neolithic (stone-age) → Chalcolithic (copper use) → Early Bronze Age → Middle Bronze Age → Late Bronze Age → Iron Age as an Old Testament format. He designates



the Neolithic as being from 8000–4000 BC. In this book he does not make any comments regarding time before the Neolithic.

He asks a question in the Introduction:

“... in what way does a study of the land of the Bible give us a greater understanding of the Bible itself? A primary purpose of archaeology and its related disciplines is to shed light on the historical and material contexts in which the events narrated in the Bible occurred. Archaeology helps to provide a life setting for the biblical texts, that is, a *Sitz im Leben* [the setting in life]” (p. 1).

He uses the invasion and conquest of Judea by Nebuchadnezzar as an example and shows a photo image of one of the ostraca sent by outlying Jewish troops that warns the people of Lachish that he, Nebuchadnezzar, was approaching them. Currid then comments that there are burn layers in most of the cities of Judea (or Judah) thought to be due to this event, and he mentions that 2 Kings 25 and 2 Chronicles 36 describe the event. He comments that one of 18 ostraca has a partial note “In the ninth (year)” which is consistent with 2 Kings 25:1 “Now it came about in the ninth year of his reign ... that Nebuchadnezzar





**Figure 1.** Tell Dan excavations

King of Babylon came, he and all his army against Jerusalem”. He feels that “All data—biblical, archaeological, and linguistic, come together to provide an accurate picture of what happened at Lachish during the destruction of Judah by the Babylonians.”

Currid concludes:

“It is our contention that the purpose of archaeology (and its related fields) is not to prove the Bible ... It helps to demonstrate that the events related in the biblical accounts actually took place (p. 3).”

He goes on to comment that this is important because our culture is both “ahistorical” and “uninformed” regarding the history of the Bible.

### **Part 1—Geography/topography**

Chapter 2 goes through the different regions of the area. For example, about Galilee, Currid notes that it is located in the northern region of ancient Israel and its climate is similar to the Mediterranean ‘wet zone’ with rainfall of about 14 inches/year. He notes that many forests grow in this area and mountains in the northern-most area are up to 4,000 ft high. Joshua captured it during his northern campaign (Joshua 11:6–15). Hazor and Dan are the northern-most cities in Galilee. He discusses the archaeology of Tell Dan in Part 2 (p. 77). In a similar fashion he discusses the Judean Wilderness, Negev, Mediterranean Coastal Plain, the Shephelah, Central Highlands,

Jordan Valley, and the Trans-Jordan (Jordan). Overall, with the maps, it gives one a sense of the land that the Jewish peoples of the Bible lived in and live in today. As before, there are questions at the end regarding this section as well.

Chapter 3 describes the history of the excavations of the “Land of the Bible”. He discusses the discovery of the Rosetta Stone, by Napoleon’s troops, which had an inscription translated into three scripts: Demotic, Greek, and Hieroglyphics. This enabled the reading of the Egyptian inscriptions. Currid reviews the research of Paul Botta and Henry Layard’s excavations in the Mesopotamian area in the 1800s (p. 29). Pilgrims and pioneers, who did topographic surveys of the land, are mentioned. Bible societies were formed as well—all in the 1800s. Tell excavations were begun in the late 1800s, e.g. Flinders Petrie’s examination of Tell el-Hesi. Other sites such as Jericho, Beth-Shemesh, Megiddo, and Gezer were begun. Repeated visits to these and other sites would occur. Increased sophistication would be developed in terms of procedures. This chapter allows one to sense the excitement of European Christians in the unfolding of information about the Bible.

Chapter 4, Tell Excavation, describes what a tell is and how they developed as communities in the past, coalesced partly for defence and local agricultural benefits. Currid briefly describes how archaeologists came to understand the structure of tells.

Chapter 5 is a brief, but longer than in the Introduction, description of the archaeological period nomenclature presently in use: Neolithic (NP c. 8000–4000 BC), Chalcolithic (CP c. 4000–3200 BC), Early Bronze Age (EBA c. 3200–2350 BC), EB IV–Middle Bronze Age I Transition (MBA c. 2350–2000 BC), Middle Bronze II Age (c. 2000–1550 BC), Late Bronze Age (LBA c. 1550–1200 BC), Iron I Period (IA c. 1200–1000 BC), and Iron II Period (c. 1000–586 BC). This chapter is helpful to the student and researcher when reviewing an archaeological report as it helps put the data into a broader context.

### **Part 2—A journey through the land**

Maps that display the geographical areas of Part 1 are included in Part 2 along with short discussions and occasional photos of key archaeological sites in each area.

Chapter 6 discusses tells in the Sea of Galilee area (figure 2). Tell Dan (pp. 76–78) is mentioned as “a 55-acre site located near the foot of Mount Hermon”. It has evidence of being inhabited in the Neolithic, EBA, MBA, and IA. It has a prominent MBA outer wall with glacis defences. It had an arched gateway as well. It is first mentioned in Genesis 14:14 in which Abram pursued men who had taken his nephew Lot captive. Jeroboam I is listed as having a cultic complex there and a golden calf. It was still a cultic center during the time of Amos (8:14)<sup>4</sup>. Per Currid, Tiglath-pileser III destroyed the city in 732 BC. Other tells mentioned include Tell Hadar on the eastern shore of the Sea of Galilee, which was inhabited in the LBA I, IA I, and IA II. Large amounts of carbonized grain were found there. Tell Hazor, “the largest tell in Palestine”, is discussed along with a brief discussion of the city structure. Tell Kedesh is mentioned as it is in an Egyptian Execration text (800–900 BC). It also was a city of refuge (Joshua 21:32). It contained MB, Persian, and Hellenistic remains. Tell Kinrot, Sha’ar Hagolan, and Tel Soreg are mentioned

as well. Each is important to an understanding of the history of the region.

Chapters 7–12 discuss tells in each of the other regions and how they associate with the history of the Jewish peoples in the land. One gets the sense of the ancient peoples living and distributed through the land.

### Part 3—Aspects of society

Chapter 13: Agriculture and Herding. The author quotes Deuteronomy 8:7–8: “For the Lord your God is bringing you into a good land, land of brooks of water, of fountains and springs, flowing out in the valleys and hills, a land of wheat and barley, of vines and fig trees and pomegranates, a land of olive trees.” In this chapter he discusses how the domestication of animals and crop growing developed. Interestingly, he comments that in the Pre-pottery Neolithic there may have been herding of ibex, then in the Neolithic/Chalcolithic domesticated cattle and swine appeared. Trades such as smelting, ivory use, and pottery use appeared in the Beersheba area. He comments that the plowshare appeared in the Bronze Age. Cereals were cultivated, and an Egyptian panel of workers winnowing is on p. 163. Querns<sup>5</sup> were used for grinding grain and have been found at archaeological sites and the process of grinding is mentioned in Isaiah 47:2. The Gezer calendar is mentioned in which the seasons for agriculture are listed. It was written in paleo-Hebrew script in about 900 BC.

Chapter 14: Water. This chapter discusses the access of water. He associates water management with agriculture and notes Jericho in the Pre-Pottery Neolithic Period PPNP (c. 8000 BC) as having some evidence for barley and emmer cultivation. Pithos jars<sup>6</sup> were developed in the PNP, then cisterns as seen at Arad were developed in the IA, then shafts to water sources, example Hazor. Currid then summarizes a discussion regarding the Hezekiah tunnel and possible Canaanite shaft in Jerusalem (p. 173). It is clear from this chapter that water



Figure 2. Sea of Galilee and upper Jordan River Valley from the Golan Heights

was essential and sometimes difficult to obtain.

Chapter 15: Architecture. Currid reviews the use of mud brick which he says was used as early as Pre-Pottery Neolithic (PPNP) at Jericho. In the Middle Bronze Age stone bases and mud brick upper layers were used and field stone throughout some walls in the IA. He comments that many of the stone walls were “rubble masonry” as stone was plentiful in the areas. Plastering of the walls did occur in the Neolithic. Fortification occurred early even in the PPNP. Temple structure may be found in the Chalcolithic at Teleilat Ghassul. Formed stone occurred in the IA and the IA gate at Megiddo and is a good example.

Chapter 16: Ceramics. Currid comments that clay had been used in walls and clay “objects” before evidence of pottery. Some of the clay had even been fired. He comments that the origin of pottery vessels is unknown, but that clay-lined fire pits have been found at Jericho. Once developed, Currid states that the pottery, in Pottery Neolithic and forward, is known for its ubiquity and durability and thus can be used to chronologically date sites. Various shapes, sizes, and decorations were then developed. It should be noted that the Philistine black and red on a white slip is very artful. The common understanding is that pottery was hand shaped in the PNP and CP then the ‘slow’ potter’s wheel<sup>7</sup> came into use at Megiddo in the EBA 1. The “fast” wheel is found in the MB II period.<sup>8</sup>

Currid talks about the importance of keeping pottery separated into groups and cleaning/washing it well.

Chapter 17: The Hebrew Language in Archaeology. Dr Currid reviews what many consider the origin of Hebrew starting with Hamito-Semitic or Afro-Asiatic. This is largely based on the conjugation of verbs. The sub-group is Semitic. The tablets found at Ebla, 2300 BC, helped to associate the vocabulary, syntax, and grammar of Canaanite, Phoenician, and Hebrew. Further understanding of the development of Hebrew has come from ostraca found in various excavations such as Khirbet Qeiyafa. The mention of Yahweh is found on an ostrakon dated 9<sup>th</sup>–7<sup>th</sup> century BC. A key inscription was the finding of the Siloam Inscription (Hebrew), composed during the digging of the tunnel for water in King Hezekiah’s day, 716–687 BC. Currid mentions 2 Kings 20:20 regarding the digging of the tunnel in Hezekiah’s day. LMLK (“belonging to the King” in Hebrew) stamped jar handles are also found throughout Israel. Other relevant ostraca that verify Jewish presence in the land are listed, including the ones at Lachish which included an intercommunication among Jewish leaders regarding the advance of Nebuchadnezzar in 588 BC. The Ketef Hinnom silver prayer scroll is listed as well. The author documents the presence of the Jewish peoples in the land by the many inscriptions of various types found there.

Chapter 18: Burial Practices. Currid comments that, “Some of the earliest known burials in ancient Palestine came from the Natufian period (c. 10000–8500 BC).” So, it is clear that he accepts an intermediate to longer age for mankind on the earth than some others.<sup>9</sup> He then goes on to review the burial practices in each of the standard archaeological periods. Probably all of the burial practices were associated with the religious views of the time period. He comments on orientation of skeletons and on a collection of skulls at Jericho that were covered with plaster (p. 218). Rock-cut tombs and anthropoid clay coffins have been found as well.

Chapter 19: Small finds. This is a collection of comments on various manufactured items such as flint tools and clay figures associated with deities in the Neolithic Period. Later bone tools appeared per Currid. Wood arrow shafts, combs occurred in later strata at Jericho. Unsmelted copper use occurred in the Neolithic Period with progression use occurring about 3000 BC and then smelted iron use about 1500 with the Hittites. Ivory from elephants and hippopotamuses came into use in the Chalcolithic Period. Glass, non-obsidian, has been found in glass beads from the EBA and vessels in the MBA. Glassblowing occurred during the Roman Period.

Currid’s appendices include #1 Basic Timeline of the Ancient Near East; #2 The Kings of Israel and Judah which helps to understand the united and divided Kingdom periods; #3 Extrabiblical References to the Kings of Israel and Judah including the *House of Dan Inscription* which mentions the house of David; the *Moabite Stone* which mentions a Moabite king’s victory over Israel in about 800 BC and many other stone inscriptions that include evidence regarding the Israel (Northern Kingdom about 800–700 BC) and Judah (Southern Kingdom about 800–600 BC) leaders and their involvement with other leaders of the region.

This is a nice summary of the inscriptions and it has several photographs to go with it;<sup>10</sup> #4 Glossary—short but helpful—for example, a favissa is “an ancient pit near or in a temple that contained sacred objects no longer in use” (p. 247).

Chapters 13–19 and the appendices give a nice review of the human aspect of living and surviving in the various areas of Judah and Israel as well as Jordan.

### Problem areas

Drawbacks to the book include: there is no mention of Noah or the Flood in the book, yet archaeological evidence exists including Mesopotamian ancient tablets and numerous ancient flood stories.<sup>11,12</sup> He was and is a major figure in the Old Testament. Also, it seems he accepts a date for mankind that extends to 10,000 years ago (p. 217) which is also not necessary nor provable.<sup>13</sup>

### Conclusion

Overall, it is a useful well-written book that gives a survey of the study and uses of archaeology and a cursory review of the history of the archaeological excavations of sites in the Middle East as they relate to the Bible. I do recommend the book as an introductory source for those wanting to learn more about biblical archaeology. As well, I am thankful for Christian academics such as Professor Currid who are helping people to understand the biblical scriptures.

### References

1. “John D. Currid (Ph.D., University of Chicago) is Chancellor’s Professor of Old Testament at Reformed Theological Seminary. He has held several expedition staff positions, including ones at Bethsaida, Carthage, and Tell el-Hesi. He also served as the director of the Tell Halif (Lahav) Grain Storage Project. Currid has authored numerous books, such as the *ESV Bible Atlas* (with cartographer David Barrett, 2010) and *Against the Gods* (2013), both published by Crossway. He also served as senior editor for the *ESV Archaeology Study Bible* (2018) and contributed the notes to the Pentateuch in that volume.” Information from the book itself.
2. According to Lita Cosner, Professor Currid has made the comment: “At the base level, the issue is the same as it has been for more than a hundred and fifty years; does one hold to the complete truthfulness of the facts reported for us in Genesis 1 and 2, and especially in the immediate creation of Adam and Eve as the first humans or not?” He appears to take a literal view of Genesis and in the same article he is listed as a young age creationist. See article: Cosner, L., New book offers comprehensive critique of theistic evolution, review of Moreland *et al.* (eds.), *Theistic Evolution: A scientific, philosophical, and theological critique*, *J. Creation* 33(1):23–25, April 2019; [creation.com/review-theistic-evolution](http://creation.com/review-theistic-evolution).
3. He has written numerous books on the Christian faith including a two-volume set on Genesis—[amazon.com/Genesis-Evangelical-Press-Study-Commentary](http://amazon.com/Genesis-Evangelical-Press-Study-Commentary) and other books such as *Against the Gods*, *ESV Bible Atlas*, *Understanding Scripture*, *Doing Archaeology*, *Habakkuk*, *Ecclesiastes* and *Numbers*.
4. “As for those who swear by the guilt of Samaria, who say, ‘As your god lives, O Dan’, And ‘As the way of Beersheba lives’, They will fall and not rise again” (Amos 8:14 NASB).
5. “... the quern, which consists of a large, flat stone on the bottom and a smaller grinding stone for the worker’s hand (called a rider).” The worker would move the smaller stone back and forth on the larger stone to grind the grain (p. 164).
6. Large jars for storage—could be used for water.
7. The slow wheelbase needed to be pushed by the hand while shaping the soft clay with the other hand.
8. The fast wheel allows the wheelbase to be kicked with the foot while using both hands for shaping the soft clay into a vessel.
9. However, in reference 3, Cosner presents Currid as believing in a *de novo* (‘immediate’) creation of Adam and Eve.
10. This includes the Prism of Sennacherib; Obelisk of Shalmaneser III with King Jehu; the Tell Dan Inscription and a royal seal of Hezekiah.
11. Epic of Gilgamesh and Epic of Atrahasis mention a flood: see [www.creation.com/gilg](http://www.creation.com/gilg); and a general review at [www.creation.com/noahs-flood](http://www.creation.com/noahs-flood).
12. [trinitysouthwest.com/product/noah-flood-account/](http://trinitysouthwest.com/product/noah-flood-account/) or [amazon.com/Noah-Flood-Account-Narrative-Representation/dp/1945750030](http://amazon.com/Noah-Flood-Account-Narrative-Representation/dp/1945750030).
13. Ages of ancient civilizations are difficult to determine, esp. pre-writing. C14 is often used to date archaeology sites but per Dr Andrew Snelling in 2017: “Specifically, we know that carbon-14 has varied in the past due to a stronger magnetic field on the earth and changing cycles in sunspot activity. So, when objects of known historical dates are dated using radiocarbon dating, we find that carbon-14 dates are accurate back to only about 400 BC”, [answersingenesis.org/geology/carbon-14/radiocarbon-dating/](http://answersingenesis.org/geology/carbon-14/radiocarbon-dating/). Dr Jake Herbert talks about assumptions in C14 dating as well: [icr.org/article/rethinking-carbon-14-dating-what-does](http://icr.org/article/rethinking-carbon-14-dating-what-does).



# A fantastical dinosaur journey

## ***The Rise and Fall of the Dinosaurs: The untold story of a lost world***

Steve Brusatte

Macmillan, London, 2018

Philip Robinson

Steve Brusatte (b. 1984) is a rising star in the world of palaeontology and dinosaurs (figure 1). He was born in the USA, but is now Reader (the second highest rank of lecturer) in Vertebrate Palaeontology at the University of Edinburgh. He has discovered many new species of fossil vertebrate. Thus, he is often looked to for some relevant quote when a new discovery in his field of expertise is found.

*The Rise and Fall of the Dinosaurs* is his eighth book and is rather adequately described as an adult pop science book, which makes it easy to digest. There are no references within the main text for the reader, but at the end of the book there are notes on the sources Brusatte used for each chapter.

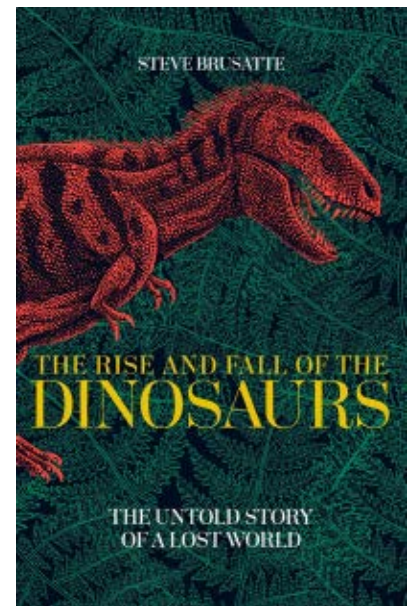
It follows a narrative style telling the reader the ‘current’ evolutionary story that Brusatte holds to, hence he must add some important disclaimers. Interwoven throughout dinosaur history are personal stories involving Brusatte, alongside a who’s who of other up-and-coming palaeontologists, as well as those firmly established as leaders in their field. These insertions read more like someone vying for credibility rather than adding anything of any genuine substance to the text. He also includes the background to a number of historical dinosaur bone hunters who are interesting in their own right.

The premise of the book is stated in the title, and, other than the (many) insertions mentioned above, the text attempts to tell the story of the dinosaurs in three phases. Their beginning, their dominance, and their extinction. All three phases are surrounded by mass extinction events. Before the book starts properly there is a dinosaur family tree included which looks more like a creationist dinosaur kind line-up (with the exception of birds) rather than an evolutionary one (figure 2). It also sums up the evolutionary depth of the book. As the family tree shows, there is no adequate precursor to the dinosaurs, and there were distinct kinds.

There are currently around 1,000 dinosaur species, which biblical creationists place in 50–55 kinds. Due to the large number of animal species, skeptics have asked how they could all have fitted on Noah’s Ark. The high numbers that this would require for dinosaurs alone is fodder for such skeptics. Brusatte explains that “A new species of dinosaur is currently being found, on average, once a week. Let that sink in: a new dinosaur every ... single ... week. That’s about fifty new species each year” (p. 6). Apart from the maths, it alludes to more going on. There appears to be a systematic failure in current palaeontology whereby even the smallest difference between dinosaurs which are obviously related<sup>1</sup> results in their being given different names, rather than being grouped together using their abundant similarities.

### **The dawn of the dinosaurs**

Brusatte is a very clear evolutionist, believing that “Rocks record history;



they tell stories of deep ancient past long before humans walked on earth” (p. 13). The story starts with a vividly described picture of the alleged Permian–Triassic (P–Tr) extinction, 252 Ma ago. Volcanoes, streams of liquid rock, explosions, eruptions, dust, ash, acid rain, a landscape scorched with lava, barren landscapes, food chains collapsing. It is claimed to be the most severe mass extinction of all, in which around 90% of all species disappeared. However, as life is resilient, it was in this gap that the scene was set for dinosaurs to make their appearance—enter the Triassic.

This is when the story gets very messy, with Brusatte trying to explain to the reader exactly how dinosaurs took advantage of the extinction, and where they came from. He never does quite get around to this and ties himself and the reader in knots when attempting to do so. The first animal we are introduced to is the 250-Ma-old *Prorotodactylus* which was identified from a trackway in Poland.

However, *Prorotodactylus* is an ichnogenus, which is a classification based solely on fossil traces such as tracks or burrows where these are deemed to be distinctive and not from



**Figure 1.** Steve Brusatte digging in Algarve, South of Portugal

a type known from other evidence. In other words, no actual physical fossils of the animal have been found. It is a problem for evolutionists that trackways are often found millions of evolutionary years before any animal that could have made them. A better explanation is that the animals left tracks while trying to escape from rising floodwaters, but then the Flood caught up and buried the creature on higher land.

Brusatte says that *Prorotodactylus* was a small, house-cat-sized, quadrupedal archosaur, belonging to the animal line from which dinosaurs allegedly came. It walked in an upright fashion with arms and legs directly underneath the body, as opposed to sprawled out beneath the body.

Until this time, the sprawlers had dominated the Permian, so he calls this transition to walking upright “a landmark evolutionary event” (p. 28). There is no explanation as to how this actually happened. “We may never know exactly why ... [they] started walking upright, but it probably was a consequence of the end-Permian extinction.”

But wait, *Prorotodactylus* is not just an archosaur, it is actually a dinosaur-morph, “a member of that group

that includes dinosaurs and the handful of their very closest cousins” (p. 31). Thus, this archosaur-cum-dinosaur-morph is actually a dinosaur? Sorry, where exactly did dinosaurs come from again? Allegedly, “At some point, one of these primitive dinosaur-morphs evolved into true dinosaurs. It was a radical change in name only. The boundary between non-dinosaurs and dinosaurs is fuzzy, even artificial” (p. 33).

From here we learn that from the study of more dinosaur-morph trackways in Poland (and others found in France, Germany, and the USA) by 246 Ma ago they are now the size of wolves and racing around on only two legs. This is stated as a fact with no attempt to explain how any such transition took place. The ‘true’ dinosaurs then arose between 240 and 230 Ma ago. But Brusatte doesn’t really know, as maybe some of the footprints made earlier than this

“... were made by real, true, honest-to-goodness dinosaurs. We just don’t have a good way of telling apart the tracks of the earliest dinosaurs and their closest non-dinosaur relatives, because their foot skeletons are so similar. But maybe it doesn’t matter too much, as the origin of the true dinosaurs was much less important than the origin of the dinosaur-morphs” (p. 34–35).

For Brusatte, trying to figure out this line between true dinosaurs and their dinosaur-morph ancestors continues to cause him ‘headaches’, but they are “ripe to be solved by the next generation of palaeontologists” (p. 34). Kicking the origin of the dinosaurs and their ancestors onto the next generation is not only exceptionally weak, but the reader is left to wonder for a man only in his mid-30’s what he will be doing for the next 20–30+ years himself.

Brusatte has already had to spend some of this time correcting his own thinking about dinosaurs during this period in evolutionary history. At the time of publication, Brusatte believed

that there were no truly gigantic sauropods that weighed over ten tons, as they didn’t reach this scale until at least 170 Ma (p. 102). However, the discovery in Argentina of a bus-sized sauropod, ‘dated’ as having lived around 210 Ma, has moved the ‘evolution’ of gigantism back tens of millions of years.<sup>2</sup> *Ingentia prima* is estimated to have been up to 10 metres (32 feet) long and weighed up to 11 tonnes. In response to the discovery Brusatte said, “I think it’s one of the most important dinosaur finds of the last few years. These new fossils force us to rethink when, and how, dinosaurs got so enormous”.<sup>3</sup> Not only does this find change evolutionists’ ideas on dinosaur evolution, it also presents them with some gigantic problems. As Brusatte believes that the first true dinosaurs, which were small (cat to wolf size), only entered the scene at the most 252 Ma ago, he now has a significantly shorter period of time to explain how these vast anatomical differences arose.

### Dinosaurs rise up

During the Triassic period, the dinosaurs quickly evolved into three major groups: theropods, long-necked sauropods, and ornithischians. Again, no mention of how these radically different body plans actually took shape. But by 200 Ma they were still relatively small in numbers compared to other species that lived at the time (p. 81). In order to mount their global revolution, there needed to be another mass extinction, called the Permian–Jurassic (Tr–J) event.

Around 201 Ma, the supercontinent Pangea breaks up. This sparks a 600,000-year reign of terror with megamonsoons—extreme seasonal changes in wetness and dryness—plus volcanoes spewing out lava. “In all, some three million square miles of central Pangea were drowned in lava” (p. 87), treacherous weather and extreme climates. In this mass extinction event over 30% of all species, and maybe

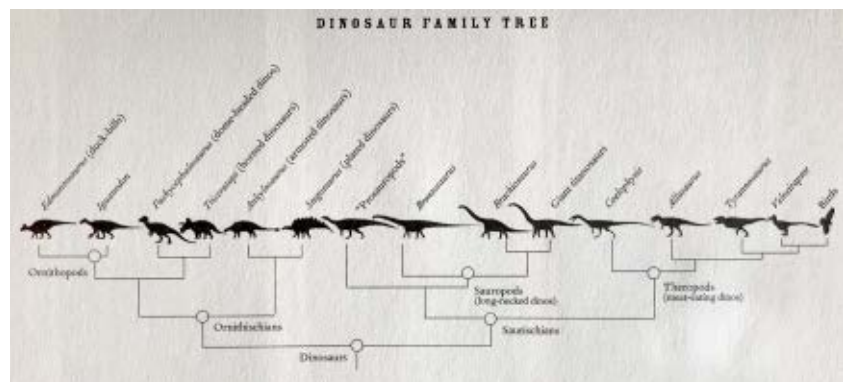
more, died out. It was this event, killing off the competition, which Brusatte claims allowed the dinosaurs to greatly diversify in response and rise to their dominant position.

“Somehow dinosaurs were the victors. They endured the Pangean split, the volcanism, and the wild climate swings and fires that vanquished their rivals. I wish I had a good answer for why. It’s a mystery that quite literally has kept me up at night” (p. 98).

But of course, rather than attempt to actually figure this out within his own evolutionary worldview, he again kicks the problem down to the next generation, stating, “Whatever the answer, it’s a riddle waiting for the next generation of paleontologists to figure out” (p. 99). There is unfortunately a very distinct pattern forming in the book in which Brusatte again tells a wonderful story but totally fails to explain any of the details. Having now firmly entered the Jurassic period, this marks the proper period of the dinosaurs’ dominance on the earth’s landscape.

## Dinosaurs die out / take flight?

The third piece of the puzzle, where the dinosaurs went after their dominant period in evolutionary history, is also explained by another familiar-sounding mass extinction event. We are again met by fantastical scenes of total catastrophe on a day some 66 Ma ago told from the dinosaur's perspective. Duckbills eating flowers, raptors chasing prey, *T. rexes* terrorizing the other dinosaurs. Some of them may have noticed a glowing orb in the sky (p. 309). That orb was a comet or an asteroid, "we aren't sure which" (p. 315), which collided with the Yucatán Peninsula of Mexico. It, "hit with the force of over 100 trillion tons of TNT, somewhere in the vicinity of a billion nuclear bombs' worth of energy" (p. 315). This event led to the extinction of some 70% of species, including all of what he calls



**Figure 2.** Dinosaur family tree (from page ix)

“non-avian dinosaurs”, over the course of a few thousand years.

Brusatte then attempts to answer the all-important puzzle of:

“Why did all the non-bird dinosaurs die at the end of the Cretaceous? After all, the asteroid didn’t kill everything. Plenty of animals made it through . . . . So what was it about *T. rex*, *Triceratops*, the sauro-pods, and their kin that made them a target?” (p. 336).

And we can add marine reptiles—the plesiosaurs and mosasaurs (the ichthyosaurs disappeared earlier, for some unknown reason).

The subsequent answer amounts to that other animals, such as mammals, being smaller and having more omnivorous diets, were able to hide in burrows and eat a greater variety of food. Or crocodiles being able to hide in aquatic ecosystems close to land, and birds being able to lay and hatch their eggs in about half the time of the dinosaurs. Dinosaurs apparently had none of these advantages, so died. That is the disappointing sum total of the evidence provided. But, of course, dinosaurs didn't really die out; part of their empire remains.

Brusatte toes the current evolutionary mainstream line, stating that “Dinosaurs are still among us today. We’re so used to saying that dinosaurs are extinct, but in reality, over ten thousand species of dinosaurs remain” (p. 271).

“There is a dinosaur outside my window. I’m watching it as I write this . . . . A real, honest-to-goodness, living, breathing, moving dinosaur . . . . The dinosaur I’m watching is a seagull . . . . Seagulls, and all other birds, evolved from dinosaurs. That makes them dinosaurs” (p. 269–271).

Brusatte accepts *Archaeopteryx* as the first true bird, ‘dated’ to be 150 Ma old, which comes arrayed in feathers. In an interesting admission Brusatte states that “If dinosaurs did have feathers, that would be the final jab in the gut to the few old-blood leftovers who didn’t accept the connection between dinosaurs and birds” (p. 279). Is this perhaps why feathered dinosaurs are so often falsely pushed and depicted?<sup>45</sup> While, of course, nothing in the creation model excludes dinosaurs from having feathers, the fossil evidence for this as of yet has been lacking.<sup>6</sup>

Brusatte presents to the reader *Sinosauropteryx* as evidence of the start of the journey showing that true non-avian dinosaurs had feathers. Surrounded by a 'dino fuzz' it was thought to display proto-feathers. However not only have these instead been shown to be partially decayed collagen fibres in skin,<sup>7</sup> but, as *Sinosauropteryx* comes 20 Ma after *Archaeopteryx*, any discussion about these alleged proto-feathers, which Brusatte calls the "earliest feathers" (p. 292), is a moot point. The reality is, as Brusatte points



out, “You need fossils to study major transitions, because they’re not the sort of thing we can re-create in the lab or witness in nature” (p. 281). While Brusatte admits that “The first flapping fliers must have originated sometime before 150 million years ago” (p. 303), there are no fossils to study this alleged major transition, which he states would have been 170–180 Ma ago. Neither is there any ancestor to the fully formed bird *Archaeopteryx* actually proposed in the book.

### Dinosaur depictions

When biblical creationists give presentations on dinosaurs, they normally show depictions of them through the past 4,000 years. For example, the late Eastern Zhou (3<sup>rd</sup> century BC) wine vessel excavated in 1975 from a tomb in Sanmenxia, Henan Province, China, demonstrates this beautifully (figure 3). There are four sauropod dinosaurs, one on each side, which may very well be depicting a *Camarasaurus*. When discussing some dinosaur footprints that Brusatte found on the Isle of Skye, Scotland, he writes:

“If I were handed a blank sheet of paper and a pen and told to create a mythical beast, my imagination could never match what evolution created in sauropods. But they were real: they were born, they

grew, they moved . . . . And there’s absolutely nothing like sauropods around today—no animals with a similar long-necked and swollen gut type body, no creatures on land that even remotely approach them in size” (p. 108).

Brusatte goes on to inform the reader that when sauropod dinosaurs were originally found, in the first half of the 1800’s, the finders were in a bind as they didn’t know what they were, thinking, due to their size, they were whale bones. If it is the case that his own imagination could not stretch to create such beasts, and that it took a number of years to figure out what the sauropod bones belonged to, then why do we have depictions of dinosaurs from every continent except Antarctica going back a few thousand years? Rather than such clear and true images coming from someone’s wild imagination, it makes much more sense that they are actual depictions of animals that people saw and interacted with. Such evidence is not considered in this book.

### Same old, same old

The rise and fall of the dinosaurs presents little new in the way of major up-to-date discoveries and fails to interact at all with the discovery of dinosaur soft tissue, which has been an established fact for over 15 years. While introducing mass extinction events for the dinosaurs’ rise, dominance, and fall, there is little to no substance for how any of these alleged events actually contributed to their history other than dumb luck that they survived the first two and were snuffed out in the third. There is no explanation at any point as to how the range of dinosaur body plans came about or changed from small animals (cat- to wolf-sized) to the huge and memorable *Tyrannosaurus rex* or *Diplodocus*. The numerous insertions about Brusatte’s own interactions with other palaeontologists feel like they are there to pad

out a made-up story that lacks any real detail.

From a biblical perspective, the mass extinction (death) events aforementioned should not be viewed as separate events as all took place during the Flood in a considerably shorter time frame. The mass fossil graveyards are testimonies to judgment by God as outlined in Genesis 6–8. And, of course, the Bible is clear that their kinds were preserved in Noah’s Ark and lived on after the Flood. That some of the animals such as dinosaurs<sup>8</sup> are not found in more modern rock layers does not mean that they did not live beyond this point. As Brusatte acknowledges, “Absence of evidence is not always evidence of absence, as all good paleontologists must constantly remind themselves” (p. 59).

While Brusatte is a good storyteller, he may fare better with creating a fantastical Hollywood film than describing the historical past. In the end, his so-called untold story just feels like the same old told (discredited) story.

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8. Or, for example, the Wollemi pine not found in rock layers below an alleged 65 million years ago, but currently growing in Australia. For more see: Sensational Australian tree . . . like ‘finding a live dinosaur’, *Creation* 17(2):13, 1995; [creation.com/woll](http://creation.com/woll).

Image: Seth Joel



**Figure 3.** Picture of a bronze wine vessel featuring an accurate depiction of a sauropod dinosaur on each side. Note the long neck and swollen gut that Brusatte refers to when describing sauropod dinosaurs. Even using Brusatte’s own logic it makes much more sense that the people who made such depictions actually saw the animals.

# Creation cosmologies, old and new

Dr Phillip Dennis devotes a great number of equations<sup>1</sup> to trying to refute the relativistic basis I derived 13 years ago<sup>2</sup> for my second cosmology, published a year later.<sup>3</sup> I feel like he is beating a fossil horse, because for the last few years I have been working on a new cosmology, a third, which has very little resemblance to my first two cosmologies.

The problem I now see with my first two is that they do not pay enough attention to how God says He made the cosmos in Genesis Chapter 1. Three verses there strongly imply that the speed of light in the heavens during the first four days of creation was very great. Chapter 1 also implies that the speed of light on Earth was normal at all times, and that the speed of light in the heavens slowed down to normal just before the end of the fourth day. I have only vague ideas about how He changed the speed of light so drastically. But none of today's creationist cosmologies, including my first two, take account of these vital facts from the Bible. I hope to publish a fuller explanation of the scriptural constraints soon.

However, it is still important to know if the relativistic basis for my

second cosmology is correct or not, because it applies to the spacetime within the 'waters above the heavens', which still exist today at great distances from us (Psalm 148:4). Let me point out some of what I think are Dennis's errors:

## 1. Continuity across boundaries is necessary

A crucial error is that he thinks solutions of Einstein's equations do not have to be continuous across their boundaries. Figure A1 from my 2007 paper shows how I disagree, claiming that the metric coefficients (such as  $g_{rr}$ ) should be continuous at two boundaries, inside and outside the mass shell. All physically possible solutions to differential equations, of which Einstein's equations are an example, must meet boundary conditions. A confusing factor here is that Dennis makes the shell have zero thickness and infinite density, a delta function, which is physically unrealistic. My solution is for a shell of finite (although small) thickness. A respected relativity textbook (to which Dennis himself refers on a different topic) says:<sup>4</sup>

"In the absence of a delta-function surface layer [at a boundary  $\Sigma$ ] ... the intrinsic geometry of  $\Sigma$  must be the same as seen from above and below,

$$g_{ij} \text{ continuous across } \Sigma \quad (21.169)''$$

The textbook equation is saying that the metric coefficients  $g_{ij}$  must be continuous across a boundary. That directly contradicts Dennis. The next item is an example of how his mistake undermines much of his thinking.

## 2. Dennis's alternative solution lacks continuity

Dennis's pair of equations (8) are his alternative solution to the mass shell problem. But they are

discontinuous at radius  $R$ , as he himself said. He saw nothing wrong with this because of his error above. So he did not look for a way to make them continuous. However, a suitable transformation of the coordinates in the first of the equations could solve the problem. Let us transform the coordinates in his first equation, which I will call eq. (8a), so that we have

$$dT^2 \rightarrow (1 + 2\Phi) dt^2 \quad (1)$$

$$dr^2 \rightarrow (1 + 2\Phi)^{-1} dr^2 \quad (2)$$

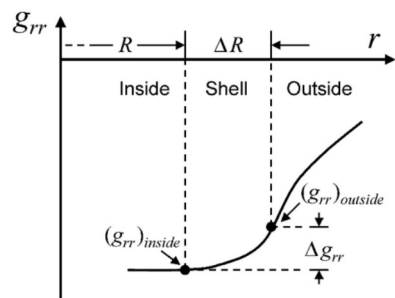
$$r^2 \rightarrow (1 + 2\Phi)^{-1} r^2, \text{ where} \quad (3)$$

$$\Phi = -\frac{M}{R} \quad (4)$$

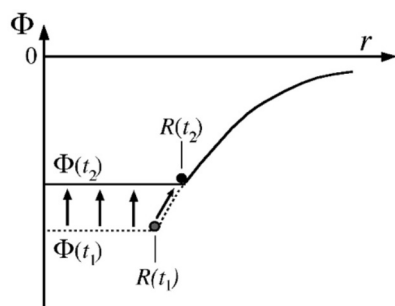
If the radius of the shell,  $R$ , is constant with time, then the transformations are merely scale changes, making them clearly valid. Then his equations (8a, b) become the same as mine, and he would have continuity inside and outside the shell. But Dennis says his eq. (8a) is supposed to be valid for  $R$  changing with time also. If a changing  $R$  makes the transformations above invalid, then he would have to find a different solution for his continuity problem here.

## 3. Potential inside an expanding shell actually changes

Dennis's continuity error leads him into a related error, a serious one. He thinks the gravitational potential inside the shell of mass does not change with time when the radius of the shell changes. I think it does. I am guided by what happens in several similar physical systems governed by similar equations. One has to do with electric potential (voltage). The second figure of my 2007 paper, which I am here calling figure A2, applies just as well to electric potential as it does to gravitational potential. It shows how the electric potential at and inside a negatively charged spherical shell would increase as one slowly (much less than



**Figure A1.** The metric coefficients must be continuous from outside to inside the shell.



**Figure A2.** Increasing (from time  $t_1$  to time  $t_2$ ) the radius  $R$  of a negatively charged shell increases the (negative) electric potential  $\Phi$  inside the shell.

the speed of light) increases the radius of the shell. This follows directly from simple electromagnetics and continuity of potential from outside to inside the shell. A voltmeter whose probes touch the outer surface and ground would register a negative voltage. That voltage would become less negative as the shell expands. However, the voltage difference between inside surface and outside surface would remain nearly zero throughout the expansion. End-note 50 of my 2007 paper discusses this situation with more technical detail and a reference to a physics journal.

Another paper of mine<sup>5</sup> discusses a two-dimensional approximation to Einstein's equations, the mathematics of a trampoline depressed by a heavy ring. The depression is flat inside the ring. If we slowly increase the radius of the ring, the depression will rise up. The fabric inside the ring would remain flat, but it would also rise up. So the depth of the depression inside



**Figure A3.** Trampoline illustrates gravitational potential.

and outside would decrease. The fabric remains continuous from outside to inside of the ring. The depth of the depression (the deviation from the fabric's position with no ring) corresponds exactly to the gravitational potential as I am using it in Einstein's equations. This analogy implies the gravitational potential is continuous from outside the spherical shell to the inside, and that the potential inside the shell increases as the radius of the shell increases.

#### 4. Dennis validates my solution for the static case

Without emphasizing the point, Dennis acknowledges that my metric, his equation (9), is an exact solution for the case that the shell radius and potential  $\Phi$  do not change with time. That was something I did not know before I did my 2007 derivation, and that was the main reason I did it. He made the point mathematically in his eqs. (10) through (15) by putting my metric into the Einstein equations and turning the mathematical crank. His eqs. (16), (17), and B(2) through B(4), give the results. The right-hand sides should be components of the momentum-energy tensor,  $T^i_j$ , the source term in the Einstein equations. I now agree with Dennis that this tensor should be zero inside the shell. Notice that if  $\Phi$  does not change with time, all the right-hand sides will be zero. That means my metric is an exact solution for the static case.

Notice that my solution is isotropic, the same in all three space directions. For it to be correct suggests that the transformation I used to make my solution isotropic, my eq. (A44) and his eq. (20), is not the 'major mathematical error' Dennis claims it is. That is probably because the time rate of change of the potential is zero in this case.

#### 5. Toward a time-dependent solution

When the time rate of change of the potential,  $\dot{\Phi}$ , is small, then the right-hand sides of Dennis's eqs. (16), (17), and B(2) through B(4) are close to zero. That would happen if the rate of change of the shell radius  $R$  were small compared to the speed of light. In that case my static solution would be a good approximation to a time-dependent solution.

But it would be helpful to have an exact time-dependent solution. Dennis's proposed alternative interior metric, eq. (8a), is not obviously time dependent. But the analogy in figure 3 suggests that a time-dependent solution exists.

Furthermore, eq. (8a) represents a flat space. But if we were to suddenly increase the radius of the ring in figure A3 at close to the speed of sound in the fabric, the fabric just inside the ring would rise before the fabric further inward would move. That would generate a wave of rising fabric moving inward toward the centre at the fabric's speed of sound. That means the fabric inside the ring would not be flat for a while, but rather slope downward toward the centre. Only after we stop the ring's outward motion, and then wait for the waves to dissipate, would the fabric inside the ring become flat again, now at a higher level.

So there are several things wrong with eq. (8a). First, it fails to connect to eq. (8b) at the shell radius  $R$ . Second, it fails to increase the potential when  $R$  increases. Third, the potential fails to have a slope when  $R$  increases rapidly.

It looks like there is something wrong with the derivation of eq. (8). Dennis's *ansatz*, eq. (1), requires  $g_{\theta\theta}$  and  $g_{\phi\phi}$  to be static and independent of  $\Phi$ . That appears to lock him into a static solution which is independent of potential. Perhaps if he had started with the isotropic initial metric he used



in his eq. (11), which has more general forms for  $g_{\theta\theta}$  and  $g_{\varphi\varphi}$ , he might have found a more realistic solution.

## 6. The mathematics needs to connect with the physics

While Dennis criticizes other things, I think I have responded to the arguments that are essential to his case. He makes serious errors, but he is correct in saying that my solution is not exact for an expanding shell. However, that is true for his alternative metric also. It falls short of being physically plausible. His proof that my static solution is exact is helpful to me, and I am grateful for that.

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## » Phillip Dennis replies:

I am glad that Dr Humphreys refers to his shell model<sup>1,2</sup> as a ‘fossil horse’ if that amounts to a public retraction of it, although he recently brought the model to my attention as recently as March 2020, in apparent approbation. I am puzzled that he dug up his fossil horse to apparently present it as a viable model. That was the impetus for my critical analysis. Furthermore, I am

aware of no published retraction of his ‘fossil horse’.

In this letter I outline the serious errors in Humphreys' reply. The full mathematical critique is available online at [creation.com/critical-analysis-in-depth](http://creation.com/critical-analysis-in-depth).

## Section 1. Continuity across boundaries is not necessary

Humphreys merely reasserts his view that metric coefficients must *necessarily* be continuous. It is true that solutions of differential equations should meet boundary conditions. But solutions also need to satisfy all conditions of the equations, including the presence of surface layers. My solution including a discontinuity at the shell surface layer has the appropriate boundary conditions at all necessary regions: at the origin, at infinity, and at the shell.

The objection to the delta function is irrelevant as my equations (39–40)<sup>3</sup> for a cavity inside a layer of mass included no delta function. That solution of the EFE shows that the interior of the cavity is Minkowski space with no ‘timeless zone’.

Another consideration is that the delta function is a concise representation of a thin shell. The delta function captures the integral of the density over the radial distance of a non-zero thickness, i.e.

$$\int \frac{M\delta(r-R)}{4\pi r^2} dV = M = \int_R^{R+\Delta R} \rho(r) dV.$$

The detailed integration of the EFE as in equations (3–5) in Dennis,<sup>3</sup> yields for Humphreys' values  $(g_{rr})_{inside}$ ,  $(g_{rr})_{outside}$ :

$$(g_{rr})_{inside} = -1$$

$$(g_{rr})_{outside} = -\left(1 - \frac{2M}{r}\right)^{-1}. \quad (1)$$

In other words, integration over the shell thickness  $\Delta R$  yields a discontinuity in *inside* and *outside* values, determined by the amount of *gravitational* mass within the shell—a contradiction of Humphreys' continuity claim. The ‘unrealism’ of the delta function is a red herring.

We return, then, to the *thin layer* representation, to which section 21.13 of MTW<sup>4</sup> is applicable. In order to support his view of metric coefficients he quotes MTW in the section on surface layers. Unfortunately, his quote indicates that he does not understand the mathematics.

Misunderstanding of MTW and the geometry of surface layers

Humphreys quotes MTW equation (21.169) as support for his claim for the necessity of the continuity of metric components. However, the quote does not support him in the manner in which he enforced continuity. A careful study of section 21.13 of MTW and an understanding of surface layers shows that Humphreys' version of metric continuity is incorrect. I agree with MTW. MTW does not “directly contradict Dennis”, rather, MTW contradicts Humphreys.

First, the MTW continuity condition concerns the *intrinsic* metric of the three-dimensional hypersurface  $\Sigma$  *containing the mass*, which for the shell is a time-like surface layer. Further, the requirement in equation (21.169) is stated in terms of a *Gaussian normal coordinate system*. In other words,  $g_{ij}$ ,  $i, j = 1, 2, 3$ , are the components of the metric tensor within the layer of matter, i.e. in a coordinate system which conforms to the surface layer. This is illustrated in figure 21.6 on page 552 of MTW.<sup>4</sup> Paying attention to these details is important in understanding surface layers in GR. It may be a surprise that my equation (8):

if  $r < R(\tau)$ :

$$ds^2 = -dT^2 + dr^2 + r^2 d\Omega^2$$

if  $r > R(\tau)$ :

$$ds^2 = -\left(1 - \frac{2M}{r}\right) dt^2 + \left(1 - \frac{2M}{r}\right)^{-1} dr^2 + r^2 d\Omega^2 \quad (2)$$

satisfies equation (21.169) which refers to embedding  $\Sigma$  with *intrinsic geometry* ( $g_{ij}$ ) in different regions of space-time with different curvatures. The embedding was performed in Appendix A of my critique.<sup>3</sup> Clearly, Humphreys did not recognize that Appendix A showed how equation (21.169) is satisfied.

The intrinsic metric of the hypersurface  $\Sigma$  is equation A(45):

$$ds^2 = -d\tau^2 + R^2(\tau)(d\theta^2 + \sin^2(\theta)d\phi^2). \quad (3)$$

The components relevant to equation (21.169) are:

$$g_{ij} = \begin{bmatrix} -1 & & \\ & R^2(\tau) & \\ & & R^2(\tau)\sin^2\theta \end{bmatrix}.$$

Equation (21.169) specifies that the metric of the surface layer is the same when ‘seen from above’ (i.e. as embedded in the Schwarzschild spacetime) and when ‘seen from below’ (i.e. as embedded in the Minkowski spacetime). A summary of Appendix A is that the metrics A(43) and A(44) must

both induce A(45) (equation (3)), i.e. that the shell metric is *isometric* to the boundary of the interior and exterior. Appendix A<sup>3</sup> showed that A(45) is continuous across  $\Sigma$ .

Humphreys is wrong since he attempts to enforce continuity (using a spurious appeal to a potential) in Schwarzschild coordinates—which do not conform to the specification of normal coordinates in the hypersurface of matter.

Humphreys says equation (2) above is in error. However, it was obtained by following the method in MTW<sup>4</sup> (p. 554) for solving the EFE in the presence of surface layers:

“In analyzing surface layers, one uses **not only** the junction conditions (21.168a) to (21.169), **but also** the four-dimensional Einstein field equation applied on each side of the surface  $\Sigma$  separately, **and also an equation of motion** for the surface stress-energy [emphases added].”

I do not deny the continuity at thin layers as explained in MTW. I deny Humphreys’ method. Humphreys’ misinterpretation of MTW is underscored by the fact that after discussing the condition (21.169), MTW gives an exercise to apply the theory. It would be remarkable that MTW would establish the continuity of the *intrinsic geometry* and then turn around and present W. Israel’s<sup>5</sup> equivalent of my equation (2)

in exercises 21.25–27 in MTW<sup>4</sup> which Humphreys claims “has a problem”—see figure 1, equations (21.176a, b). If I have a ‘problem’ then so do world-renowned general relativists MTW and W. Israel<sup>5</sup>.

## Section 2. My solution appropriately lacks continuity in curvature coordinates

Humphreys takes me to task for presenting a solution with non-continuous coefficients. However, stating this is a ‘problem’, since it runs counter to his thesis is question begging. Per section 1, my equation *does have continuity!* *It is not of the mistaken type that Humphreys claims.*

He then presents a transformation that supposedly reinstates continuity of the metric coefficients for a static shell. He says this transformation makes my solution equivalent to his metric. Humphreys’ external isotropic metric is not a solution of the EFE. Since the exterior is a vacuum, the Ricci scalar  $R$  should be zero. However, the computed value from his metric is:<sup>6</sup>

$$R = -\frac{6M^2}{2Mr^3 - r^4}, \quad (4)$$

proving it is not a solution of the EFE. Thus, his putative transform is irrelevant.

A more telling test would be to try to make my (2a) continuous with (2b), both of which are solutions of the vacuum EFE.

Applying Humphreys’ transformations yields:

if  $r < R$ :

$$ds^2 = -\left(1 - \frac{2M}{R}\right) dt^2 + \left(1 - \frac{2M}{R}\right)^{-1} dr^2 + \left(1 - \frac{2M}{R}\right)^{-1} r^2 d\Omega^2$$

if  $r > R$ :

$$ds^2 = -\left(1 - \frac{2M}{r}\right) dt^2 + \left(1 - \frac{2M}{r}\right)^{-1} dr^2 + r^2 d\Omega^2$$

Thus, equation (2) does not become the same as his. While this restores continuity to  $g_{tt}$  and  $g_{rr}$ , it destroys

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21. VARIATIONAL PRINCIPLE AND INITIAL VALUE DATA

$$ds^2 = -dt^2 + dr^2 + r^2(d\theta^2 + \sin^2\theta d\phi^2) \text{ inside,} \quad (21.176a)$$

$$ds^2 = -\left(1 - \frac{2M}{r}\right) dt^2 + \frac{dr^2}{1 - 2M/r} + r^2(d\theta^2 + \sin^2\theta d\phi^2) \text{ outside.} \quad (21.176b)$$

Let the “radius” of the shell, as a function of proper time measured on the shell, be

$$R \equiv \frac{1}{2\pi} \times (\text{proper circumference of shell}) = R(\tau). \quad (21.176c)$$

Show that the shell’s mass density varies with time as

$$\rho(\tau) = \mu/4\pi R^2(\tau), \quad \mu = \text{constant} = \text{“total rest mass”}; \quad (21.176d)$$

and derive and solve the equation of motion

Figure 1. Excerpt from Misner, Thorne, and Wheeler (MTW)<sup>4</sup>

continuity of  $g_{\theta\theta}$  and  $g_{\phi\phi}$ , the very components that are required for continuity of the *intrinsic geometry* of the shell hypersurface as in MTW.<sup>4</sup> His erroneous transform has led him to further false analysis.

Another indication that his transformation is erroneous is that it changes the metric signature from  $(+, -, -, -)$  to  $(-, +, +, +)$ . This error is the root of his *tri-temporal zone*. *A coordinate transform cannot change the signature of the spacetime metric. This signature change should have raised a red flag.*

To summarize, Humphreys endeavoured to fit my correct interior solution to his erroneous exterior metric. When the attempt is made to fit the interior solution to the correct exterior solution (i.e. eq. (8b)) we find that Humphreys' scale transformation makes the metric discontinuous. Humphreys' claim, "If a changing  $R$  makes the transformations above invalid, then he would have to find a different solution for his continuity problem here", is false.

Contra Humphreys, I have no continuity problem and I need no different solution.

### Section 3. There is no 'Newtonian potential'—inside a shell it does not change

Humphreys repeats his electromagnetic and potential analogy without validation. Since the analogy leads to equations that are not solutions of the EFE that is a sufficient rebuttal of his 'analogical approach'. Further, Humphreys now admits that a time-dependent potential is not a solution, so how can the 'potential' change?

Discontinuous metric coefficients are not the 'serious error' that he claims. The serious error is Humphreys'. His isotropic metric is not a solution.

The trampoline model refutes Dr Humphreys

After reasserting his potential analogy, he adduces a trampoline to

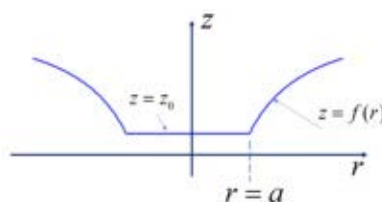


Figure 2. Profile function of a trampoline

illustrate his concepts. He declares this model to *exactly* represent his potential model. He states:

"The depth of the depression (the deviation from the fabric's position with no ring) *corresponds exactly* to the gravitational potential as I am using it in Einstein's equations. This analogy implies the gravitational potential is continuous from outside the spherical shell to the inside, and that the potential inside the shell increases as the radius of the shell increases [emphasis added]."

This is merely a claim; no analytical demonstration is provided. The trampoline surface corresponds to the 'fabric of space', not to a potential. The trampoline model actually refutes Humphreys.

Mathematical model of a trampoline

Figure 2 shows the profile of a trampoline of radius  $a$ . The trampoline is generated by rotating the profile  $z = f(r)$  about the  $z$ -axis. The trampoline surface is embedded in 3D Euclidean space. The metric interval for Euclidean space in cylindrical coordinates is:

$$ds^2 = dr^2 + r^2 d\phi^2 + dz^2 \quad (5)$$

Using standard calculus, the trampoline metric is:

$$\begin{aligned} ds^2 &= \left[1 + (f')^2\right] dr^2 + r^2 d\phi^2 \\ &\equiv g_{rr} dr^2 + g_{\phi\phi} d\phi^2 \end{aligned}$$

$$g_{rr} = \begin{cases} 1 & \text{if } r < a \\ 1 + (f')^2 & \text{if } r \geq a \end{cases}$$

This is manifestly discontinuous for  $f' \neq 0$ . Thus, contra Humphreys, the trampoline proves that  $g_{rr}$  is discontinuous.

### Section 4. My solution does not validate Humphreys' solution for the static case

Contra Humphreys I have not validated his isotropic solution for *any* case. *Checking the solution* by substitution is a proper method to validate solutions. If Humphreys had checked his exterior metric, as in equation (4), he would have seen that *his isotropic exterior metric is not a solution*.

I pointed out that Humphreys' exterior metric is not a solution. My equations (18–19)<sup>3</sup> are the correct exterior isotropic solution derived in textbooks.

Constant radius is not a solution

The Israel equation of motion<sup>5</sup> shows that Humphreys' claim of a constant  $R$  solution is incorrect. Israel<sup>5</sup> derived the equation for the acceleration of the shell:

$$\ddot{R} \left[ (1 + \dot{R}^2)^{1/2} + \left( 1 - \frac{2M}{R} + \dot{R}^2 \right)^{1/2} \right] = -M(1 + \dot{R}^2)/R^2 \quad (6)$$

For constant radius,  $R = R_0 > 2M$  and  $\dot{R} = 0$ , this implies:

$$\ddot{R} = -\frac{M}{R_0^2} \left[ 1 + \sqrt{1 - \frac{2M}{R_0}} \right]^{-1}.$$

Since  $\ddot{R}$  is negative the shell collapses.

Incredibly, Humphreys claims that his violation of tensor transformation laws is not a major mathematical error. He claims this by an appeal to his isotropic form, *which is not a solution*. His equation A(44) with a time-dependent coefficient is most certainly an error. It is obvious that for constant  $R$  the function  $f(t)$  in equation A(44)



is not a function of time. Then, A(44) would reduce to a valid transformation:

$$d\bar{r}^2 = kdr^2.$$

That is not Humphreys' time-dependent equation A(44), nor would it yield his isotropic metric.

In summary, Humphreys' transformation is a serious mathematical error. That error results in an erroneous metric, inducing a 'tri-temporal' signature change—a 'solution' he still references approvingly in his reply. Committing mathematical errors that result in metrics that do not solve the EFE is a major error no matter how much Humphreys says otherwise.

### Section 5. We already have time-dependent solutions

In my critique I presented a time-dependent solution of the EFE with an interior cavity in equation (40)<sup>3</sup> which follows from the EFE in comoving coordinates.<sup>7,8</sup> That equation shows the cavity is Minkowski space with no *timeless zone*.

Additionally, equation (2) is an exact time-dependent solution. The time dependence occurs in the radius  $R = R(\tau)$ . Equation (2) is the solution presented in exercises 21.25–27 of MTW,<sup>4</sup> and derived by W. Israel<sup>5</sup> in his seminal paper.

### Section 6. Humphreys' mathematics is flawed and does not connect with the physics

In his concluding section Humphreys claims he has answered the main concerns. This most certainly is not true. Ironically, he says the "mathematics needs to connect with the physics", when his mathematics is flawed and does not connect with physics. First, he has failed to address the issue of the pathological signature change and the 'tri-temporality' of his interior metric—a universe of

one-dimensional beings evolving in three temporal directions. Second, there are no 'timeless zones'.

### Conclusions

In summary, Humphreys' errors are:

- Not understanding section 21.13 of MTW. His quote of equation (21.169) as supporting his continuity claim is mistaken.
- Failing to check his isotropic metric.
- Claiming  $R = \text{constant}$  is a solution, although the equation-of-motion derived from the EFE shows it is not.
- Adducing another faulty analogy with the trampoline.
- Erroneously asserting without proof that my equation (2) is not a solution.

None of his claims of 'serious errors' in my shell solution are true. His reason is merely that it disagrees with his erroneous potential continuity conjecture.

Finally, Humphreys did not reply to the criticism of his 'timeless zones' and 'tri-temporality'. The 'timeless zones' emerged from his erroneous metric, his misunderstanding of metric signatures and the Schwarzschild ' $t$ ' coordinate. In private communication Humphreys has informed me that he now agrees with the GR community that  $t$  for  $R < 2M$  is not time. That is tantamount to a retraction of the conclusions of *Starlight and Time* (S&T)<sup>9</sup> and also of 'a critical potential' that creates 'timeless zones' in his potential model. Rejection of those conclusions invalidates his claims of a solution to the light travel time problem.

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# Amphibian responses to the 1980 eruption of Mount St Helens—implications for Noahic Flood recovery

Keith H. Swenson

Noah's Flood was the greatest ecological disturbance in Earth history, and yet Earth's biota subsequently recovered, demonstrating remarkable resilience. In similar manner, the 1980 eruption of Mount St Helens in Washington State, USA, severely disrupted a large ecosystem, the responses of which have been, and continue to be, observed and documented. General mechanisms of disturbance and principles of recovery have been delineated, which likely apply to other large disturbances, including Noah's Flood. Therefore, lessons learned at Mount St Helens should assist biblical creationists in constructing a model for post-Noahic Flood biological recovery. This article looks at one facet of the Mount St Helens eruption, the impact on amphibians, and their subsequent responses to disturbance, including the following topics: mortality, biological legacies, persistence, dispersal, soil enrichment, colonization, predation, and resilience. Implications for a post-Noahic Flood recovery model are discussed.

On May 18, 1980, Mount St Helens, a stratovolcano in Washington State, USA, erupted, producing a 570 km<sup>2</sup> severely disturbed landscape.<sup>1,2</sup> This 'blast zone' has, over the last 40 years, proven to be a world-class laboratory for the study of biological responses to catastrophic ecological disturbance. Researchers in the new discipline of Volcano Ecology<sup>3</sup> have suggested that lessons learned at Mount St Helens are not only applicable to other volcanic settings, but also likely apply to various types of catastrophic disturbances.<sup>4</sup> Such thinking encourages biblical creationists to use lessons learned at Mount St Helens as an aid in developing a model for post-Noahic Flood recovery.<sup>5-7</sup>

This article considers the responses of amphibians to the eruption of Mount St Helens. Attention is given to pre-disturbance amphibian species and their habitats, the impact of the disturbance on amphibians, and amphibian responses to the disturbance. Implications for understanding biological recovery following Noah's Flood are discussed.

## Amphibian biology

All amphibian species (fossil and living) are included in the class Amphibia. Extant Pacific Northwest amphibians occupy two orders: Caudata (salamanders) and Anura (frogs/toads).<sup>8</sup> Both orders are divided into several families.<sup>9</sup>

'Amphibian' means 'double life', referring to life cycles which contain both aquatic and terrestrial components.<sup>10</sup> Amphibians in the Pacific Northwest include several species of salamanders, frogs, and toads. Typically, they lay gelatinous egg masses in aquatic settings, which produce aquatic larvae. After variable periods of time, larvae complete

metamorphosis, resulting in reproductively mature terrestrial adults, which return to water to breed.<sup>11</sup>

Amphibian skin is unique among vertebrates.<sup>10</sup> It is 'naked' in that it is not covered by scales, feathers, or fur. Two types of skin glands are generally present: one which produces a thin mucous film that keeps the skin moist<sup>12</sup> and another which manufactures skin toxins that defend against predators. Amphibian skin is also quite porous, readily allowing passage of atmospheric gases and water. Gas exchange through the skin supplements lung function. Four species at Mount St Helens are actually lungless, relying solely on cutaneous respiration.<sup>13</sup> Most amphibians readily lose water through their skin, as well as absorb it. Cutaneous water loss necessitates a moist environment for most species.

Amphibians are ectothermic ('cold-blooded'), that is, their body temperature is regulated by the environmental temperature.<sup>10</sup> They also alter their internal temperature through behaviour. For example, in hot weather, some amphibians cool by entering underground burrows. Many amphibians survive winters beneath insulating forest debris or buried in the mud bottoms of ice-covered ponds or lakes.

Larval salamanders are carnivores, feeding on zooplankton and other minute organisms, while anuran tadpoles are largely herbivorous, consuming primarily algae.<sup>14</sup> As adults, all Northwest amphibians prey on insects, other invertebrates, and occasionally small vertebrate animals.

## Pre-disturbance amphibian habitats and species

Prior to its 1980 eruption, Mount St Helens was a 2,950 m ASL (above sea level) stratovolcano located on the west side

**Table 1.** Fifteen amphibian species found at pre-eruption Mount St Helens, along with their preferred breeding habitats. Order Caudata (salamanders) contains 10 species (in 4 families), and Order Anura (frogs/toads) has 5 species (also in 4 families).

Order	Family	Organism		Habitat
Caudata	Ambystomatidae	Northwestern salamander	( <i>Ambystoma gracile</i> )	lake, pond
		Long-toed salamander	( <i>Ambystoma macrodactylum</i> )	lake, pond
		Cope's giant salamander	( <i>Dicamptodon copei</i> )	stream
		Coastal giant salamander	( <i>Dicamptodon tenebrosus</i> )	stream
	Rhyacotritonidae	Cascade torrent salamander	( <i>Rhyacotriton cascadae</i> )	seep
	Salamandridae	Rough-skinned newt	( <i>Taricha granulosa</i> )	lake, pond
	Plethodontidae	Larch Mountain salamander	( <i>Plethodon larselli</i> )	forest
		Van Dyke's salamander	( <i>Plethodon vandykei</i> )	forest
		Western Red-backed salamander	( <i>Plethodon vehiculum</i> )	forest
		Ensatina	( <i>Ensatina eschscholtzii</i> )	forest
Anura	Leiopelmatidae	Coastal tailed frog	( <i>Ascaphus truei</i> )	stream
	Bufo	Western toad	( <i>Anaxyrus boreas</i> )	lake, pond
	Hylidae	Pacific treefrog	( <i>Pseudacris regilla</i> )	lake, pond
	Ranidae	Red-legged frog	( <i>Rana aurora</i> )	lake, pond
		Cascades frog	( <i>Rana cascadae</i> )	lake, pond

of the Cascade Mountain Range in the state of Washington, USA.<sup>15</sup> Its summit and upper slopes were seasonally clad with deep snowpack and also supported a dozen glaciers. Tundra and alpine meadows occupied high and medium elevation sites. Below timberline, and extending onto the surrounding landscape, grew expansive old-growth, plantation, and recently clear-cut conifer-dominated forests. Several mountain lakes, the largest being Spirit Lake, were clustered to the north. Fast-flowing streams draining the area emptied into the Columbia River system. The climate was Pacific maritime and temperate, with a mean annual precipitation of 2,373 mm at an elevation about 1,000 m ASL. Within this setting existed numerous amphibian habitats, including forests, meadows, seeps, ponds, lakes, and streams.

The pre-eruption amphibian assemblage at Mount St Helens was determined largely from museum collections, historical records, and surveys done soon after the eruption.<sup>16</sup> The results include 10 salamander and 5 frog/toad species (table 1).

### The disturbance and its results

The 1980 eruption of Mount St Helens consisted of diverse volcanic processes which interacted with a pre-disturbance landscape, forming a mosaic of disturbance zones (figure 1).<sup>17</sup> A gradient of disturbance was established, extending from areas near the mountain, where intense processes eliminated

all pre-eruption organisms, to distant sites, where limited disturbance allowed survival of most organisms. Five volcanic processes formed disturbance zones:<sup>17</sup>

1. Debris avalanche: the initial massive landslide composed of the summit and north slope of Mount St Helens.
2. Directed (lateral) blast: a northward, ground hugging steam explosion that destroyed 570 km<sup>2</sup> of forest in less than 10 minutes.
3. Vertical eruption: a 9-hour upward eruption producing a continuous rain of ash and pumice (tephra) on the Mount St Helens area and beyond.
4. Pyroclastic flows: incinerating flows which formed the Pumice Plain located directly north of the mountain.
5. Mudflows (lahars): flows of melted snow and glacial ice, along with volcanic debris, that travelled down streams draining Mount St Helens.

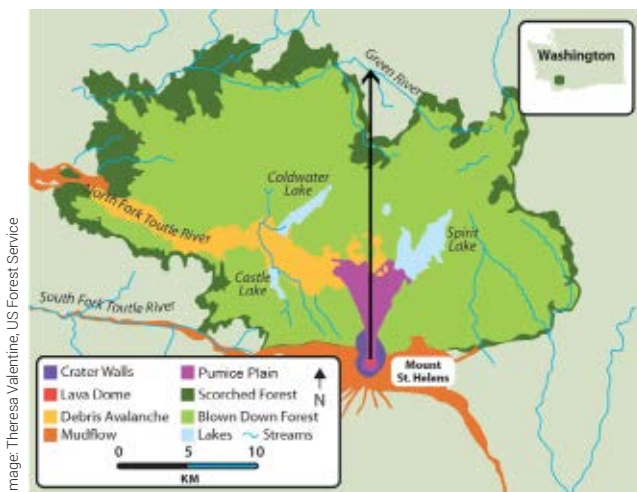
The complex landscape produced by these processes forms the stage on which the drama of biological responses is playing.

### Amphibian responses to the disturbance

1. Amphibians experienced high mortality

There are no reliable estimates of the number of amphibians which perished in the 1980 eruption of Mount St Helens,





**Figure 1.** Map of the blast zone showing disturbance zones, including: debris avalanche deposit, forest blowdown zone, scorch zone, Pumice Plain, and mudflow deposits. The arrow represents a gradient of disturbance, which depicts a progressive decline in disturbance intensity between the Pumice Plain and the intact forest.

but the toll must have been great. Amphibians in the devastated area were subjected by volcanic processes to high-impact forces, extreme heat, abrasion, deep burial, the suspension of particulates in aquatic systems, and possibly chemical toxicity.<sup>18,19</sup>

It is likely that three species of woodland salamanders were completely extirpated from the blast zone. These were the western red-backed salamander (*Plethodon vehiculum*) Larch Mountain salamander (*Plethodon larselli*), and ensatina (*Ensatina eschscholtzi*) – all members of the family Plethodontidae (lungless salamanders).<sup>20</sup> Plethodontids live on the forest floor, which provides less insulation from volcanic impacts than does an aquatic habitat, especially ice-covered lakes and ponds. In addition, no red-legged frogs were found in early surveys, suggesting there were no survivors of this species either.<sup>21</sup>

## 2. Amphibians became biological legacies

However, despite high mortality, many amphibians survived the eruption. Amphibians were first reported in the blast zone in the summer of 1980.<sup>22</sup> Subsequent surveys indicated that 11 of the 15 pre-disturbance species survived the eruption.<sup>21</sup> These became known as ‘biological legacies’, a term coined at Mount St Helens for all biological material, both living and dead, that persisted into the post-disturbance period.<sup>18,23</sup> It became apparent that the types, amounts, and distributions of amphibian legacies were a major determinant of the rate and pattern of post-eruption amphibian responses.

The timing of the eruption was critical to amphibian survival.<sup>24</sup> On May 18, winter snowpack still blanketed higher elevations around Mount St Helens and many lakes remained ice-covered. Amphibians, buried in mud at the bottom of



**Figure 2.** Northwestern salamanders persisted in ponds and lakes by becoming reproducing adults, while retaining aquatic features, including gills. This allowed them to avoid potentially lethal conditions in the surrounding landscape.

lakes, under or within coarse woody debris, or in underground burrows, were protected. Such locations (termed ‘refugia’) allowed many adult and larval amphibians to survive the eruption. Aquatic sites, especially ice-covered ponds and lakes, produced greater amphibian survival than did terrestrial habitats.

## 3. Amphibians persisted in disturbed habitats

Amphibians which survived the eruption (living biological legacies) emerged into highly disturbed aquatic and terrestrial habitats. Many perished due to unfavourable conditions, but some persisted, and even thrived. One process enabling certain salamanders to accomplish this was neoteny.

Neoteny (also called ‘paedomorphism’) refers to the retention of larval features in adult organisms.<sup>25</sup> For example, larval salamanders normally lose their fins and gills as they metamorphose into reproductively mature terrestrial adults. However, in neoteny, larval aquatic features are permanently retained throughout adulthood, requiring neotenes to live their entire lives as obligate aquatic organisms. Neotenic behaviour was observed in three salamander species following the eruption: northwestern salamanders (*Amphystoma gracile*) (figure 2), coastal giant salamanders (*Dicamptodon tenebrosus*), and Cope’s giant salamanders (*Dicamptodon copei*).<sup>26</sup>

For certain salamander species, neoteny is obligatory<sup>27, 28</sup> but for others (including those at Mount St Helens) it is facultative, occurring only under certain environmental conditions. Sprules<sup>29</sup> hypothesized that facultative neoteny may be an adaptation enabling certain salamander species to survive severe terrestrial disturbances. That is, they are able to complete their entire life cycles (including reproduction) in protected aquatic sites, thus avoiding potentially lethal conditions in the surrounding disturbed terrain.

According to Crisafulli *et al.*:

“Neoteny was an important life-history characteristic for three salamander species that appeared to allow these species to persist (or flourish) in the post-eruption landscape. Neoteny was presumably favoured because metamorphosing animals perished under harsh terrestrial conditions. As forests return to the Mount St Helens landscape, the importance of neoteny should diminish and metamorphism may become a more adaptive trait.”<sup>20</sup>

#### 4. Many (but not all) amphibian species dispersed great distances

Lengthy dispersal over harsh, barren volcanic surfaces seems a daunting task for amphibians, which are covered by a relatively delicate integument, require a continuously cool and moist environment, have specific food requirements, and travel rather slowly. Yet, many frog, toad, and salamander individuals managed to cover remarkable distances through some of the most disturbed terrain in the blast zone.<sup>30</sup> Successful dispersers colonized new ponds formed by the eruption, as well as defaunated existing habitat.

Dispersal distances for amphibians at Mount St Helens were determined between 1980 and 2000, either by tracking marked animals, or by computing travel distances from the nearest known source populations.<sup>30</sup> All results were based on a straight line of travel from the source population to the distant point of capture. Actual distances would have been significantly greater, however, since amphibians travel an irregular route due to obstacles and uneven microtopography.

Despite their seeming liabilities, amphibians at Mount St Helens made many impressive dispersal journeys.<sup>30</sup> Two western toads (*Anaxyrus boreas*) travelled at least 1.6 and 4.5 km; two Cascades frogs (*Rana cascadae*) moved 0.75 and 1.2 km; and many recently metamorphosed northwestern salamanders dispersed over 2 km. Two additional northwestern salamanders dispersed 1.9 and 3.0 km from Spirit Lake to the Pumice Plain, the most devastated part of the blast zone. Northwestern salamanders, Pacific treefrogs (*Pseudacris regilla*), red-legged frogs (*Rana aurora*), and Cascades frogs dispersed 3.7 km onto the debris avalanche deposit from their closest known source populations, while western toads and rough-skinned newts (*Taricha granulosa*) travelled 5.7 km from their nearest sources. Pacific treefrogs, observed in the volcano’s crater, accomplished the longest recorded dispersal of 10 km, from their nearest known surviving population (figure 3).

How were these remarkable journeys accomplished? Several important factors were found to determine the rate and pattern of dispersal, including high reproductive capability, species vagility, landscape permeability, and linkages with fossorial animals.<sup>30</sup>

Amphibians produce large numbers of eggs, larvae, and dispersing newly metamorphosed individuals. For example,

a mature female western toad may lay over 17,000 eggs in a single season<sup>31</sup> (figure 4), a Pacific treefrog produces 500–1,000 eggs per season<sup>32</sup>, the egg mass of a northern red-legged frog is composed of 750–2,000 eggs,<sup>33</sup> and a northwestern salamander egg mass usually contains 50–200 eggs.<sup>34</sup> Following the eruption, some amphibians experienced population booms. Ponds and streams produced abundant algae and zooplankton due to removal of the forest canopy. This provided a good food source for amphibian larvae. Also, in the early post-eruption period, there were few predators. The resulting abundance of dispersing juveniles offset the high mortality associated with dispersal and helped ensure numerous successful dispersals, despite a large number of failed attempts.

Amphibian species differ in their abilities to disperse significant distances. For example, anurans generally travel more rapidly than salamanders.<sup>35</sup> Some salamanders, such as plethodontids, have low vagility, and are termed ‘sedentary’. At Mount St Helens, these salamanders (western red-backed, Larch Mountain, ensatina) have yet to repopulate areas from which they were extirpated. Crisafulli *et al.* state:

“We predict that ensatina and western red-backed salamanders will colonize from the margins of the scorch zone and then move inward toward the core of the Pumice Plain. The Larch Mountain salamander should colonize at a much slower rate, if at all.”<sup>20</sup>

In contrast, western toads, Pacific treefrogs, red-legged frogs, and northwestern salamanders display greater vagility and are capable of more rapid and longer distance dispersals.

A major factor in amphibian dispersal is landscape permeability.<sup>36</sup> For much of the year, substrates (pumice deposits and developing soil) at Mount St Helens are impermeable to amphibians, not allowing them to cross. This includes winter, with deep snowpack, and summer, when conditions are hot and dry. However, there are two times each year when Mount St Helens’ landscapes become permeable, that is, sufficiently cool and wet for amphibians to traverse. The first is an approximate 6-week period in spring, when all substrates are saturated with water from melting winter snowpack and frequent rain events. This is when most successful dispersals take place. The second time the landscape becomes permeable is after the summer drought, with the onset of autumn rains and cool weather. Permeability at this time, however, is less reliable, because the first autumn precipitation may be a limited rain event, sufficient to initiate dispersal, but not adequate to sustain dispersing animals until they reach suitable habitat. These ‘false starts’ often leave large numbers of stranded amphibians, such as northwestern salamanders, to die from heat and desiccation. At other times, the first autumn precipitation arrives as snow, also not conducive to successful dispersion.

Another aid to amphibian dispersal in Mount St Helens’ harsh landscape is an extensive ‘subway’ system constructed by northern pocket gophers (*Thomomys talpoides*).<sup>36, 37</sup> Many of these fossorial rodents survived the 1980 eruption



**Figure 3.** The Pacific treefrog holds the record for the longest amphibian dispersal at Mount St Helens. Individuals travelled 10 km from their source area into the volcano's crater!

in underground burrows (living biological legacies). They flourished in the post-eruption environment and expanded their tunnel systems throughout much of the blast zone. Western toads, Pacific treefrogs, Cascades frogs, and northwestern salamanders have been observed accessing gopher burrow entrances, as well as openings where Roosevelt elk (*Cervus canadensis roosevelti*) tracks have broken into the tunnel system. In addition to being a travel route, this underground habitat provides dispersing amphibians with a respite from hot, dry surface conditions. In summer, tunnels are more humid and have temperatures 5–15°C cooler than on the surface.<sup>36</sup>

#### 5. Dispersing amphibians enriched developing soil

Newly emplaced volcanic substrates at Mount St Helens served as parent material for soil development. However, these deposits contained only minimal levels of nitrogen<sup>38</sup> and phosphorous,<sup>39</sup> elements required by plants and other organisms. One supply source for these needed nutrients was the ongoing 'rain' of insects and other arthropods from the atmosphere ('arthropod fallout').<sup>40,41</sup> In addition, mosquitoes were found to ferry nutrients from the waters of Spirit Lake to the nutrient-deficient pumice plain.<sup>42,43</sup>

Unsuccessful amphibian dispersers from Spirit Lake<sup>44</sup> also transported nutrients onto nearby volcanic surfaces. Studies indicated that in 2014 over 100 g of nitrogen and 12 g of phosphorous were removed by amphibians from Spirit Lake.<sup>45</sup> An undetermined percentage of these nutrients was added to surrounding pumice deposits by decomposition of unsuccessful dispersers. A small amphibian biomass has also been removed and distributed by amphibian predators, including common garter snakes (*Thamnophis sirtalis*), river otters (*Lontra canadensis*), mink (*Neovison vison*), and various birds.<sup>46</sup>

The above nutrient quantities are small, in part because less than 20% of Spirit Lake's shoreline provides adequate habitat for amphibians.<sup>47,48</sup> However, combined with dispersal from numerous other habitats, both within and outside of the blast zone, amphibians play at least a minor role in the enrichment of volcanic soils.

#### 6. Amphibians colonized suitable habitat

To be successful, dispersing amphibians must reach suitable habitat, such as ponds, streams, wetlands, meadows, and forests. At Mount St Helens, much pre-disturbance amphibian habitat was destroyed by the eruption, while other areas, although severely altered, were still able to support amphibian populations. In addition to eliminating existing amphibian habitat, the eruption created an even greater amount of new habitat.<sup>49</sup> Ground water and precipitation filled low areas between hummocks on the debris avalanche deposit, producing new ponds, 130 of which existed in 2000.<sup>50</sup> About half of these were ephemeral, drying by late summer, and half, perennial, containing water year-round. In addition, the debris avalanche dammed streams, forming new lakes, many of which breached their sediment dams and were short-lived.<sup>50</sup> Two (Coldwater Lake and Castle Lake) were stabilized by the US Army Corps of Engineers and exist today.

Post-eruption streams, ponds, lakes, and other sites, once they became geologically stable, were rapidly colonized by aquatic and terrestrial vegetation, which further stabilized substrates. These habitats provided ideal colonizing sites for dispersing amphibians. Even ephemeral ponds provided good breeding habitat for amphibians with a sufficiently short development period.<sup>51</sup>

Another source of new amphibian habitat was the activity of American beaver (*Castor canadensis*).<sup>36</sup>

None of these large rodents survived the eruption, but as riparian vegetation recovered along blast zone streams, beaver literally 'ate' their way into the devastated area. Once established, beaver dammed outlet streams of many lakes and ponds, which elevated water levels and flooded surrounding vegetation, particularly willow (*Salix* sp.) and alder (*Alnus* sp.). This greatly increased ovipositioning sites<sup>52</sup> available to reproducing northwestern salamanders, western toads, and Cascades frogs. Woody plants, cut by beaver, fell into ponds and provided additional ovipositioning structure.<sup>53</sup>

#### 7. Predators controlled amphibian populations

Prolific reproduction, abundant larval food supplies, and limited predators, pathogens, and parasites produced some remarkable amphibian population booms in the early years following the eruption. One account describes a scientist hiking in the blast zone, about a year after the eruption, seeing a hillside that appeared to be in motion. Approaching closer, he saw that the slope was totally covered by thousands of western toads, all hopping toe-to-toe!<sup>54</sup> Similar hordes of Pacific treefrogs, rough-skinned newts, and northwestern salamanders were seen at other sites. Such masses of amphibians were often short-lived due to inadequate terrestrial food sources. Eventually, boom – bust population dynamics diminished, especially as amphibian predators were established—three of which are especially notable.





**Figure 4.** Western toad larvae (tadpoles) blacken the shores of ponds and lakes within the blast zone (left), resulting in large numbers of recently metamorphosed toadlets (right).

Common ravens (*Corvus corax*) rapidly dispersed into the blast zone. These highly intelligent birds have been observed to flip toads onto their backs, strike them with their beaks, and extract the fleshy portion for food, while leaving behind the poisonous skin turned inside-out, along with the skull and eggs.<sup>52</sup>

Common garter snakes (*Thamnophis sirtalis*) became abundant about 10 years after the eruption.<sup>24</sup> These reptiles, which are semi-aquatic, have been observed feeding on adult western toads, Pacific treefrogs, and Cascades frogs, as well as larvae of western toads and coastal tailed frogs. In addition, terrestrial adult northwestern salamanders have been extracted from captured snakes.

Also found in the blast zone is the rough-skinned newt, which produces an extremely potent skin toxin.<sup>55, 56</sup> Its only known predator is the common garter snake, which is often resistant to the newt's toxin. It is likely that this predator-prey interaction has been re-established.

Brook trout (*Salvelinus fontinalis*), a non-native species, were introduced into high mountain lakes near Mount St Helens for recreational fishing from 1913 until 1979.<sup>24</sup> These lakes, formed during the Ice Age by montane glaciers, initially were fishless. They provided good habitat for amphibian species until the introduction of trout. Since brook trout feed on amphibian larvae and adults, their presence decimated amphibian populations. In May of 1980, ice cover on high mountain lakes enabled trout in many lakes to survive the eruption. Studies showed the abundance of northwestern salamanders to be about 10 times greater in lakes without fish compared to those in which fish survived.<sup>24</sup>

#### 8. Amphibians displayed great resilience

'Resilience' refers to the ability of an ecosystem, or its components, to effectively recover from disturbance. Such a 'bounce-back' was clearly observed among amphibians at Mount St Helens. Although seemingly fragile creatures and subjected to massive mortality, amphibians responded remarkably to the eruption by surviving, persisting, dispersing, and colonizing both defaunated and new habitat.

### Implications for post-Noahic Flood amphibian recovery

The new discipline of 'volcano ecology' focuses upon the effects of volcanic eruptions on ecosystems and the ensuing geophysical and biological responses.<sup>3, 57</sup> General principles derived from these studies are applicable, not only to other volcanic events, but to a wide range of catastrophic disturbances. A publication of the US Forest Service reads: "The in-depth ecological research on Mount St Helens and at other volcanoes is enabling researchers to identify universal themes in ecosystem response to disturbance" and "This means the lessons learned here can be relevant in other disturbance settings."<sup>58</sup> Such pronouncements encourage biblical creationists to use Mount St Helens' research as an aid in understanding ecological responses to Noah's Flood.

An important issue is whether amphibians survived the Flood as 'Ark kinds' or as biological legacies in the Flood waters (or both). The Bible states: "Everything on the dry land in whose nostrils was the breath of life died" (Genesis 7:22). This would include most adult amphibians, but not larvae or neotenic adults,<sup>26</sup> both of which are fully aquatic, having gills, not nostrils. In addition, several amphibian species spend over one year in their embryonic (egg) and larval stages before completing metamorphosis.<sup>59</sup> These could remain fully aquatic for the 371 days of the Noahic Flood. As freshwater fish survived the Flood, so possibly could have some larval and neotenic amphibian species.

Efforts are underway to delineate the 'ark kinds' (amphibian baramins) for extant amphibians.<sup>60-62</sup> Hennigan has tentatively<sup>63</sup> identified 53 extant Caudate kinds<sup>61</sup> and 138 extant Anuran kinds.<sup>62</sup> Of these, 6 Caudate kinds and 4 Anuran kinds are represented at Mount St Helens. Following Noah's Flood, amphibian kinds would have dispersed over the earth from the Ark, and diversified, forming post-Flood amphibian species. In addition, if larvae or neotenic adults<sup>64</sup> survived in the floodwaters, they would have dispersed from multiple sites of survival. As species, rather than kinds, their potential for further diversification would be limited. Possibly, some extant

amphibian species are descendants of Flood water legacies, rather than Ark kinds.

One specialized amphibian at Mount St Helens warrants comment. The coastal tailed frog (*Ascaphus truei*) is highly adapted to cold, fast-flowing mountain streams.<sup>65</sup> For example, its ‘tail’ (in males) is actually a copulatory organ, needed for internal fertilization in turbulent stream environments. Although Hennigan tentatively postulates a “tailed frog kind”, he acknowledges that the taxon may be a product of “post-Flood diversification from other terrestrial anurans.”<sup>66</sup> Alternatively, since tailed frog larvae have a long period of development,<sup>59</sup> and are adapted to surviving turbulent aquatic environments, it is possible that they survived in floodwaters outside the Ark.

After the Flood, surviving amphibian species, faced daunting challenges as they dispersed into and colonized a hostile environment—a situation analogous to that encountered by amphibians in the blast zone at Mount St Helens. Lessons learned from amphibians at Mount St Helens likely apply to dispersing amphibians as they repopulated the post-Flood earth. For example, neoteny possibly provided a mechanism for certain caudates to persist in harsh post-Flood terrestrial environments.

Dispersal distances of several kilometres for individual amphibians at Mount St Helens are impressive and would enable populations of amphibian Flood water legacies, beginning at multiple sites, to gradually claim large areas. However, Ark kinds faced a much more monumental task of populating the earth from one initial location, the Mountains of Ararat. How could that happen?

Certainly, the ability to rapidly disperse is highly dependent on a species’ innate vagility. Although we do not know how vagile the amphibian Ark kinds were, we can suspect that God would have preserved animals with good dispersal capability.<sup>67</sup> An illustration of how rapidly a highly vagile amphibian can claim a large area is that of the Cane toad (*Bufo marinus*) in Australia. In 1935, cane toads, native to Central and South America, were released in northern Queensland to control beetles attacking sugar cane crops. Within 10 years, the toads spread 2,000 km to Brisbane, which is a rate of 200 km per year!<sup>68</sup>

Dispersing post-Flood amphibian populations were aided by numerous other factors. High reproductive capability, abundant food sources, and limited predation likely produced population booms, as witnessed at Mount St Helens. Large floating vegetation mats<sup>69,70</sup> (such as on Spirit Lake at Mount St Helens), driven by prevailing winds and ocean currents, likely transported amphibians. The post-Flood Ice Age,<sup>71</sup> due to lowering of sea levels, produced land bridges, providing global access for dispersing man and animals.<sup>72</sup> A cool, wet Ice Age climate likely maintained permeable landscapes for amphibian travel. Linkages with fossorial animals (such as the northern pocket gopher at Mount St Helens) perhaps provided

protected passageways. Beaver, by damming streams, probably created amphibian habitat, including ovipositioning sites. And eventually, an increase in predators (along with parasites and pathogens) would have helped stabilize amphibian populations.

## Conclusion

The overarching recovery theme at Mount St Helens is that of great resilience. Ecosystems appear designed to rapidly and effectively respond to catastrophic disturbances. This observation lends credibility to global recovery, within a biblical timeframe, from Earth’s greatest ecological cataclysm, that of Noah’s Flood. Amphibians certainly played an important role in that response.

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- Exceptions in the Pacific Northwest include the rough-skinned newt, which has dry, granular skin and the western toad with dry warty skin.
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22. Karlstrom, E.L., Amphibian recovery in the North Fork Toutle River debris avalanche area of Mount St Helens; in: Keller, S.A.C., (Ed.), *Mount St Helens: Five years later*, Eastern Washington University Press, Cheney, WA, p. 334, 1986.
23. Dale and Crisafulli, ref. 19, p. 4.
24. Crisafulli, Trippe, Hawkins, and MacMahon, ref. 16, p. 196.
25. Jones, L.L.C., Leonard, W.P., and Olson, D.H. (Eds.), *Amphibians of the Pacific Northwest*, Seattle Audubon Society, Seattle, WA, p. 224, 2005.
26. Crisafulli, Trippe, Hawkins, and MacMahon, ref. 16, p. 185.
27. Cope's Giant Salamander is considered by some a semi-obligate neotene since it rarely metamorphoses in nature.
28. An example of an obligatory neotenic salamander is the common mudpuppy (*Necturus maculosus*) of the eastern United States.
29. Sprules, W.G., The adaptive significance of paedogenesis in North American species of *Ambystoma* (Amphibia: Caudata): a hypothesis, *Canadian J. Zoology* 52:393–400, 1974.
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31. Jones, Leonard, and Olson, ref. 25, p.162.
32. Jones, Leonard, and Olson, ref. 25, p. 174.
33. Jones, Leonard, and Olson, ref. 25, p. 178.
34. Jones, Leonard, and Olson, ref. 25, p. 30.
35. Dale, Swanson, and Crisafulli, ref.1, p. 194.
36. Crisafulli, Trippe, Hawkins, and MacMahon, ref. 16, p. 195.
37. Crisafulli, C.M., MacMahon, J.A., and Paramenter, R.R., Small-mammal survival and colonization on Mount St Helens Volcano: 1980–2002; in: Dale, Swanson, and Crisafulli, ref.1, pp. 199–218.
38. Engle, M.S., *Nitrogen and Microbial Colonization of Volcanic Debris on Mount St Helens*, Masters Thesis, Washington State University, Pullman, WA, 1983.
39. Newly deposited volcanic rock contains phosphorous, but a period of weathering is required for it to become available to plants.
40. Edwards, J.S. and Sugg, P.M., Arthropods as pioneers in the regeneration of life on the pyroclastic-flow deposits of Mount St Helens; in: Dale, Swanson, and Crisafulli, ref. 1, pp. 129–131.
41. Swenson, ref. 6, pp. 25–27.
42. Edwards and Sugg, ref. 40, p. 136.
43. For the first two years following the eruption, Spirit Lake contained a nutrient-rich organic soup of cooked vegetation supporting a massive bloom of micro-organisms. It subsequently returned to its normal low nutrient (oligotrophic) state.
44. Five amphibian species have dispersed from Spirit Lake, including: northwestern salamander, rough-skinned newt, Pacific treefrog, western toad, and Cascades frog.
45. Gavel, J.E., Crisafulli, C.M., and Miller, R., The new Spirit Lake: changes to hydrology, nutrient cycling, and biological productivity, in; Crisafulli and Dale, ref. 19, pp. 89–91, 2018.
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47. Adequate amphibian habitat for lake breeding amphibians consists of a shallow littoral zone, as opposed to steep cliffs which produce deep water at the shoreline.
48. Gavel, Crisafulli, and Miller, ref. 19, p. 91.
49. Before 1980, the amphibian study area contained over 30 lakes, with a collective surface area of 662 ha. The same area, after the eruption, included over 163 ponds and lakes with a surface area of 1,679 ha (an increase of 253%). See: Crisafulli, Trippe, Hawkins, and MacMahon, ref. 16, p. 185.
50. Swanson and Major, ref 1, p. 42.
51. For example, western toads need 1–3 months to complete metamorphosis, so ephemeral ponds suffice. In contrast, northwestern salamanders usually spend their first year in larval form and metamorphose in their second summer. Thus, they require perennial ponds or lakes. See: Jones, Leonard and Olson, ref. 25, pp. 33, 165.
52. Ovipositioning sites usually consist of woody twigs, partially or fully submerged in water, to which amphibians attach gelatinous egg masses.
53. In contrast, beaver dams on other streams caused loss of habitat for coastal tailed frog larvae, which require fast-flowing water, rather than placid pools. See: ref. 36.
54. Carson, R., *Mount St Helens: The eruption and recovery of a volcano*, Sasquatch Books, Seattle, WA, p. 91, 1990.
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63. Hennigan cautions concerning Caudates: “In no way is this the final word and much baraminological research must be done to improve the precision of these estimates.”; Hennigan, ref. 61, p. 17.
64. Hennigan suggests that neoteny in salamanders of the family Ambystomatidae developed only after the Flood; Hennigan, ref. 61, p.21.
65. Jones, Leonard, and Olson, ref. 25, pp. 154–157.
66. Hennigan, ref. 62, pp. 339–340.
67. Fully terrestrial woodland salamanders (ensatina, western red-backed, Larch Mountain) at Mount St Helens are very sedentary. They have no larval phase, do not metamorphose, and have no need to migrate to aquatic reproduction sites. They very likely arose by post-Flood differentiation of Ark kinds.
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# Hierarchical clustering in dinosaur baraminology studies

Matthew Cserhati, Brian Thomas, and Joel Tay

A recent baraminology study places the bird species *Archaeopteryx lithographica* together with the terrestrial dromaeosaurid theropod *Velociraptor mongoliensis*. This despite the two species being created on Day 5 and Day 6 of Creation Week, respectively. This data set was entropy-filtered and re-analyzed, yet the same error persisted. To correct this, the distance matrix from the BDIST results of the filtered data sets were transformed into a proximity matrix and *hierarchical* clustering was applied to it. This way *A. lithographica* clustered away from theropod dinosaurs such as *V. mongoliensis*, together with other bird species such as *Anchiornis huxleyi* to form a bird cluster. Using two separate data sets, one or two tyrannosaurid clusters were predicted. One more theropod cluster, as well as a dromaeosaurid, troodontid, and oviraptor cluster, was predicted as well as the family Ornithomimidae. These clusters can be viewed as putative baramins.

Genesis describes flying creatures (עוף, or “oph” in Hebrew), such as bats and birds, separately from terrestrial animals, such as most reptiles created on Day 5 and Day 6 of Creation Week, respectively. Reptiles are defined as mainly terrestrial animals that lack feathers and hair, and also have scaly skin and lay soft-shelled eggs. Since God created these two distinctly demarcated animal groups on separate days, they necessarily must belong to separate baramins, because they are the results of separate creative acts of God. Pterosaurs are flying reptiles, so they would have been created on Day 5 of Creation Week, together with birds and bats. Conversely, several bird species do not fly, such as rails and ostriches. These birds may either have been created to be incapable of flight, or, more likely, lost flight capability altogether.

A relatively recent baraminology paper by McLain *et al.* using the BDIST algorithm incorrectly lumped the bird species *Archaeopteryx lithographica* into the same cluster with terrestrial animals, such as dinosaurs, for example *Velociraptor mongoliensis*.<sup>1</sup> *Archaeopteryx* has the anatomy of a flying bird, thus it was created on Day 5. Therefore, it cannot be classified as a terrestrial dinosaur.

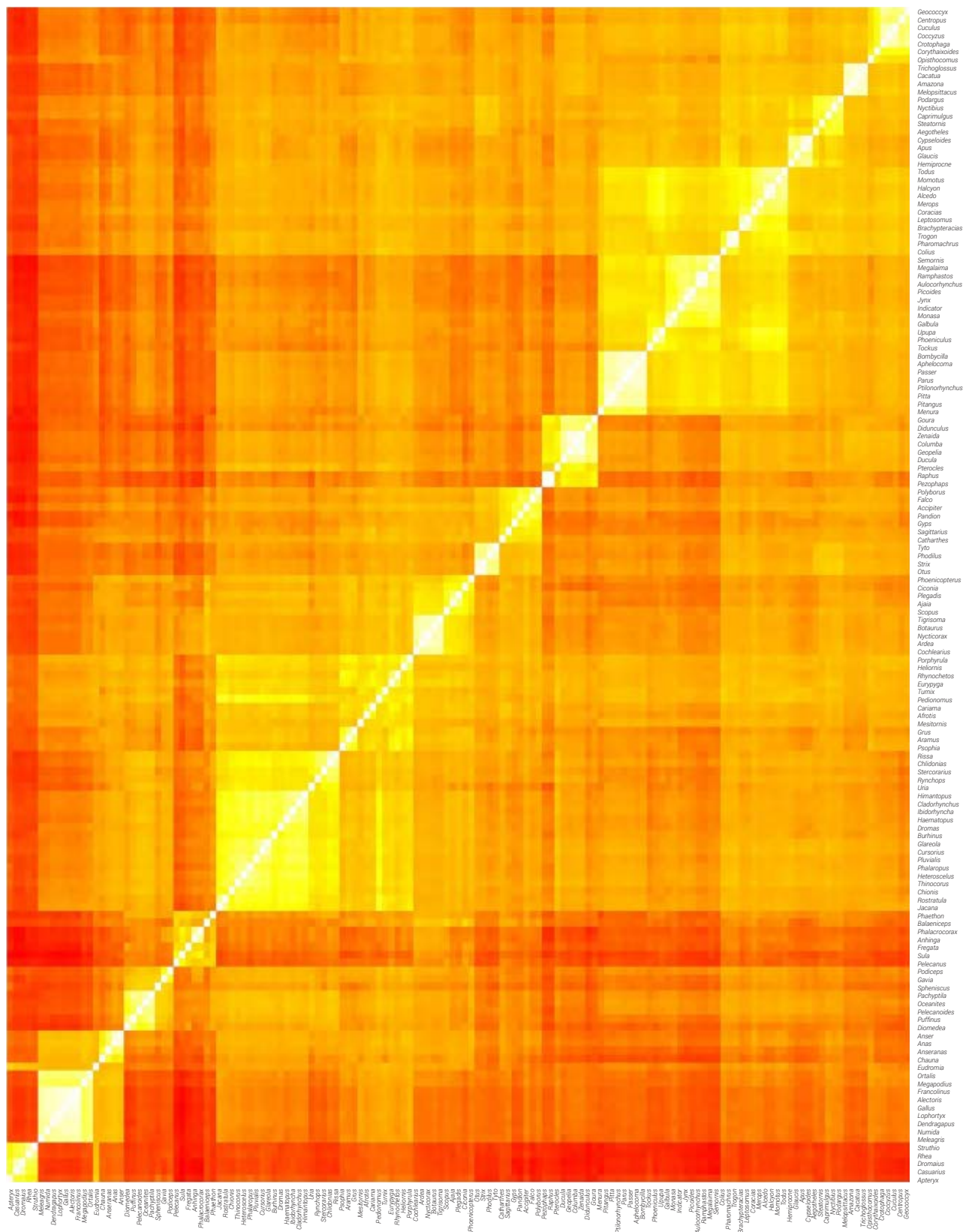
It is highly unlikely that *V. mongoliensis* also would have had feathers, even though some scientists point to bony knobs on its ulna as quill knobs.<sup>2</sup> An alternative and defensible position suggests that these tiny structures on *Velociraptor* are unlikely to be quill knobs, but rather are attachment sites for anchoring tendons or connective tissue. They are more shallow, more irregularly spaced, smaller in proportion to body size, and positioned elsewhere on the ulna than living bird quill knobs. Figure 1A, in Turner reference 2, compares the ulnae of *Velociraptor* and turkey vulture (part C of the figure). Quill knobs are not necessarily indicative of feathers—they

are possible indicators of a *particular type of flight*. Only certain flying birds that experience high stress while flying require quill knobs. For example, the albatross lacks them due to its gliding style of flight.

Pennaceous feathers have never been found buried together with *V. mongoliensis* or *Dakotaraptor*, meaning that it is unlikely that they would have had quill knobs on the bones of their forearms.<sup>3</sup> Some non-avian vertebrates also have knobs which serve as attachment points for structural elements such as fascia. Quill knobs appear in certain birds which undergo high-stress flying. The quill knobs of *Dakotaraptor* are ovoid and irregularly shaped, and are also unevenly spaced.<sup>4</sup> The quill knobs of *Dineobellator* are also broad, rounded, and irregularly spaced, as opposed to the quill knobs of *Cathartes* (turkey vulture), seen in part C of figure 1 of Jasinski, 2020.<sup>5</sup>

What many scientists believe is evidence for protofeathers in dinosaurs falls short under scrutiny. After more careful examination, filamentous structures in the skin of *Sinosauropteryx* proved to be parts of a unified structural element—possibly a crest which runs from the neck down to the tail.<sup>3</sup> Even a ceratopsian dinosaur, *Psittacosaurus*, and the heterodontosaurid *Tianyulong* had such filamentous elements, even though these species are ornithischians, which are not in the alleged lineage of dinosaurs evolving into birds.<sup>6</sup> Such collagen fibres, called pycnofibres, are also present on the membrane-like wing structures of several pterosaurs, such as *Jeholopterus* and *Nemicolopterus*. However, such structures would cause drag during flight for these creatures, and accelerate heat dissipation when wet due to rain. In comparison, bats also have membranous, hairless wings and need to expend more energy heating themselves in the rain.<sup>6</sup>

The discovery that seemingly identical structures have also been found in pterosaurs has caused some to assume



**Figure 1.** Heat map of proximity matrix derived from the BDIST analysis of the filtered Livezey and Zusi data set. Lighter colours represent proximity values close to 1, denoting species within the same baramin. Darker colours represent proximity values close to 0, denoting species from different baramins.

that pterosaurs were also covered in a dense feathery covering, but this does not explain why they are also found in marine creatures. These pterosaur ‘pynofibres’ are very likely just collagen and keratin structures in their partially degraded state. Pynofibres are indistinguishable from what some identified as protofeathers in dinosaurs. Conversely, if these pterosaurs were not feathered, neither were dinosaurs.<sup>7</sup>

One of the problems with feathered dinosaur claims is that partially decayed skin collagen is often mistaken for downy feathers. Lingham-Soliar’s two-volume work, *The Vertebrate Integument*, is widely regarded as the most detailed work on the taphonomy of integumentary structures. He demonstrates that similar fuzzy structures have been found on decaying sharks and dolphins and even fossilized marine reptiles and flying reptiles. “All reported cases of protofeathers in dinosaurs, marine reptiles, and flying reptiles alike, show a striking similarity to the structure and levels of organization of dermal collagen. The proposal that these fibres are protofeathers is dismissed.” Thus, while creationists may hypothesize that *Velociraptor* had volant ancestors, and thus created on Day 5, this has to be much better established.

#### Overview of the BDIST method and hierarchical clustering

The BDIST method is a morphology-based baraminology algorithm, which quantitatively compares the similarities and differences between the traits of a set of input species.<sup>8</sup> The algorithm calculates the baraminic distance between any two species in the following way:  $d_{ij} = m_{ij}/n_{ij}$ , where  $n_{ij}$  is the number of comparable characteristics between species  $i$  and  $j$ ,  $m_{ij}$  is the number of mismatching characteristics, and  $d_{ij}$  is the distance between the two species.

As a hypothetical example, if we compare 100 characteristics for a horse and a zebra, two animals from the same baramin, we’ll find that they differ in only five characteristics, thus  $d_{\text{horse,zebra}} = 5/100 = 0.05$ . If we compare a horse with a lion, we’d find bigger differences, let’s say 40. Thus the distance  $d_{\text{horse,lion}} = 40/100 = 0.4$ . These distance values are then put into a matrix, which can then be analyzed by clustering algorithms, such as the k-means algorithm, which belongs to the family of hierarchical clustering algorithms.<sup>9</sup>

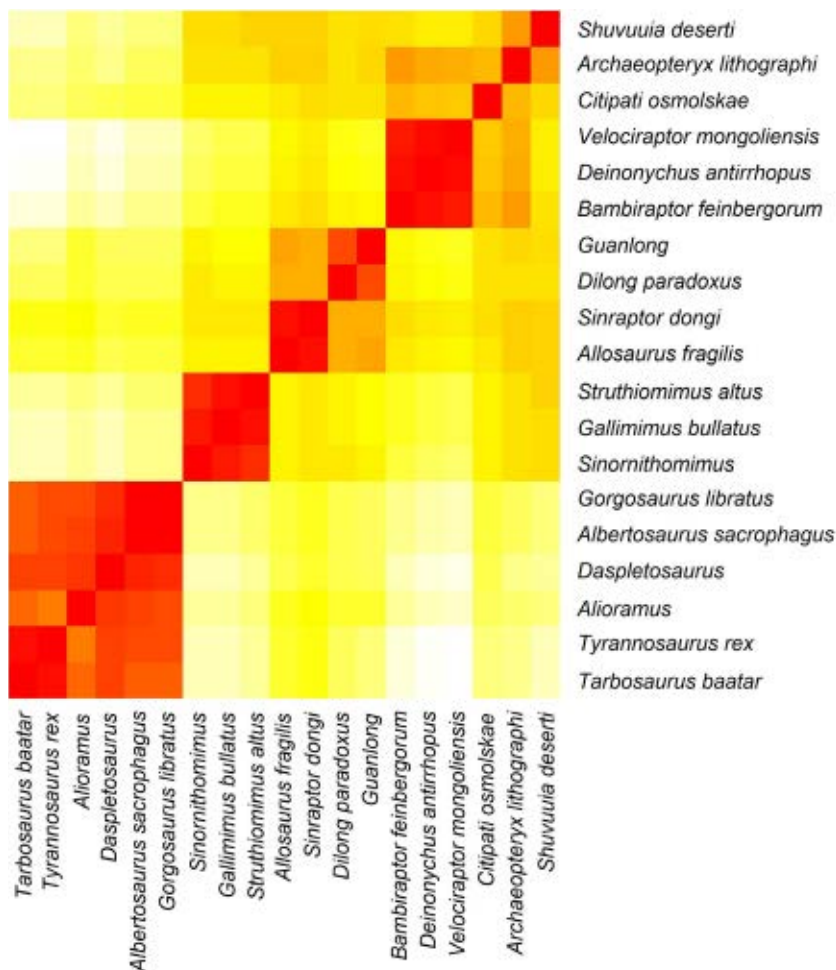
**Table 1.** List of putative clustering, which is the result of hierarchical clustering of the proximity matrix, derived from the entropy-filtered data set of Livezey and Zusi

cluster	species	min	mean	max	stdev	p-value
5 (Coraciiformes)	5	0.897	0.921	0.967	0.023	2.09E-11
6 (Galliformes)	7	0.922	0.955	0.981	0.017	2.11E-33
7 (Psittaculidae)	4	0.957	0.962	0.967	0.004	1.60E-28
11 (Passeriformes)	7	0.936	0.955	0.98	0.012	1.17E-48
13 (Apodiformes)	4	0.904	0.929	0.967	0.022	7.23E-07
15 (Ardeidae)	5	0.933	0.947	0.967	0.011	1.12E-16
16 (Piciformes)	7	0.878	0.91	0.984	0.024	5.54E-26
20 (Caprimulgiformes)	3	0.884	0.891	0.904	0.011	3.33E-04
22 (Palaeognathae cluster)	4	0.869	0.898	0.953	0.035	3.02E-06
24 (Cuculiformes)	5	0.9	0.927	0.959	0.022	7.42E-12
26 (Ciconiiformes)	7	0.863	0.896	0.95	0.022	6.20E-24
27 (Charadriiformes I)	4	0.861	0.9	0.948	0.028	6.11E-06
29 (Charadriiformes II)	5	0.867	0.902	0.942	0.025	1.51E-10
31 (Columbidae)	4	0.938	0.958	0.981	0.021	1.29E-07
48 (Procellariiformes)	3	0.918	0.929	0.946	0.015	6.42E-04
50 (Strigiformes)	4	0.917	0.936	0.976	0.023	7.12E-07

Hierarchical clustering involves partitioning a set of  $N$  entities, such as species, into  $K$  partitions (clusters), where  $1 \leq K \leq N$ . Hierarchical clustering methods fall into one of two main categories: bottom-up (or agglomerative) or top-down methods. The result of bottom-up algorithms is a nested hierarchy of clustered entities. Top-down approaches involve optimally splitting all the entities into  $K$  clusters.

Each hierarchical clustering method uses a dissimilarity and a linkage function to cluster the data. Dissimilarity functions are used to calculate the distance between the entities. These functions include squared Euclidean distance, Manhattan distance, or  $1 - |PCC|$ , where PCC stands for the Pearson Correlation Coefficient. In this way, the distance measurement (or a derivation thereof) used by the BDIST algorithm can be used in further analyses using a hierarchical clustering algorithm. The linkage function dictates how pairwise entities (species, clusters or both) are connected to one another to form clusters.<sup>10</sup> Linkage functions include Ward’s algorithm, single, complete, and average linkage.





**Figure 2.** Heat map of the proximity matrix from the BDIST results of the filtered Brusatte data set. Lighter colours represent proximity values close to 1, denoting species within the same baramin. Darker colours represent proximity values close to 0, denoting species from different baramins.

The relationships and distances between entities can be depicted on a dendrogram. The number of clusters can be determined by cutting branches at a certain height in the dendrogram. In baraminology, these clusters ideally correspond to the created kinds. Other algorithms, such as *k*-Means or PAM (Partition Around Medoids) clustering, can be used to cluster species hierarchically. The *k*-Means algorithm is a vector quantization method that is frequently used for cluster analysis by grouping objects since it quickly finds the centres of the clusters. The algorithm prefers groups with low variance and similar size. The PAM algorithm discovers objects called medoids, that are centrally located in clusters. The algorithm tries to minimize the distance between the objects and their closest medoid.

#### Previous studies and goal

Another baraminology methodology paper, which applied data filtering based on entropy measurement, attempted to

correct this over-clustering tendency in some of the data used by McLain *et al.*<sup>11</sup> It helped resolve baramins into more anatomically sensible (less inclusive) groupings, but it did not separate *A. lithographica* from terrestrial dinosaurs in two data sets from Lee *et al.*<sup>29</sup>, Brusatte *et al.*<sup>12</sup>, van der Reest *et al.*<sup>13</sup>, and Lamanna *et al.*<sup>14</sup>

Over-clustering and misclustering may result from two different causes. The first cause may be due to the use of pre-filtered data sets obtained from evolutionary studies. When creating data sets, individual characters may be chosen, and values may be assigned to them based on one's presuppositions. Evolutionary data sets might emphasize certain traits which support one or another evolutionary trajectory. For example, bird feathers may be conflated with dinosaur dermal collagen.<sup>15</sup> Therefore, if biased data goes in, we get biased results from the algorithm, regardless how well it was programmed.

It is extremely difficult—even impossible—to solve this problem, because it would involve manually evaluating and filtering possibly several hundred characters over dozens of species. However, the data set may be improved using an entropy-filtering algorithm. In addition, we can try to

alleviate this problem by using a different clustering algorithm than the one used by BDIST.

The goal of this study is to apply another clustering algorithm in an attempt to get more accurate results from analyzing the filtered data sets of the previous baraminology study. The algorithm is outlined in the Materials and Methods section, followed by the results.

## Materials and Methods

### Data

Distance matrixes were built following the methods of Brusatte, van der Reest and Lamanna studies<sup>12–14</sup> and the results of this study are available on github ([github.com/csmaty/EntropyFilter2](https://github.com/csmaty/EntropyFilter2)). The Livezey and Zusi data set is available at [morphobank.org/index.php/Projects/DownloadProjectPage/project\\_id/510](http://morphobank.org/index.php/Projects/DownloadProjectPage/project_id/510). It was downloaded

and recoded from letter characters to numerals (i.e. a=1, b=2, etc.) for use in the BDIST algorithm.

All supplementary data files are available online at [github.com/csmaty/dino\\_reanalysis](https://github.com/csmaty/dino_reanalysis). The Cytoscape file for creating figure 5 (dino\_baramins.cys) is also available at this web address.

## Methods

The proximity matrix was derived using the following simple equation:

$$p_{i,j} = 1 - d_{i,j}$$

where  $d_{i,j}$  stands for the baraminic distance between two species  $i$  and  $j$  as calculated by the BDIST algorithm, and where  $p_{i,j}$  is the corresponding proximity value for the same two species. This transformed matrix was visualized as a heatmap with the ‘heatmap’ command in R, using the ‘average’ clustering method. The ‘cutree’ command was used to determine clusters for the data sets based on the estimated number of clusters.

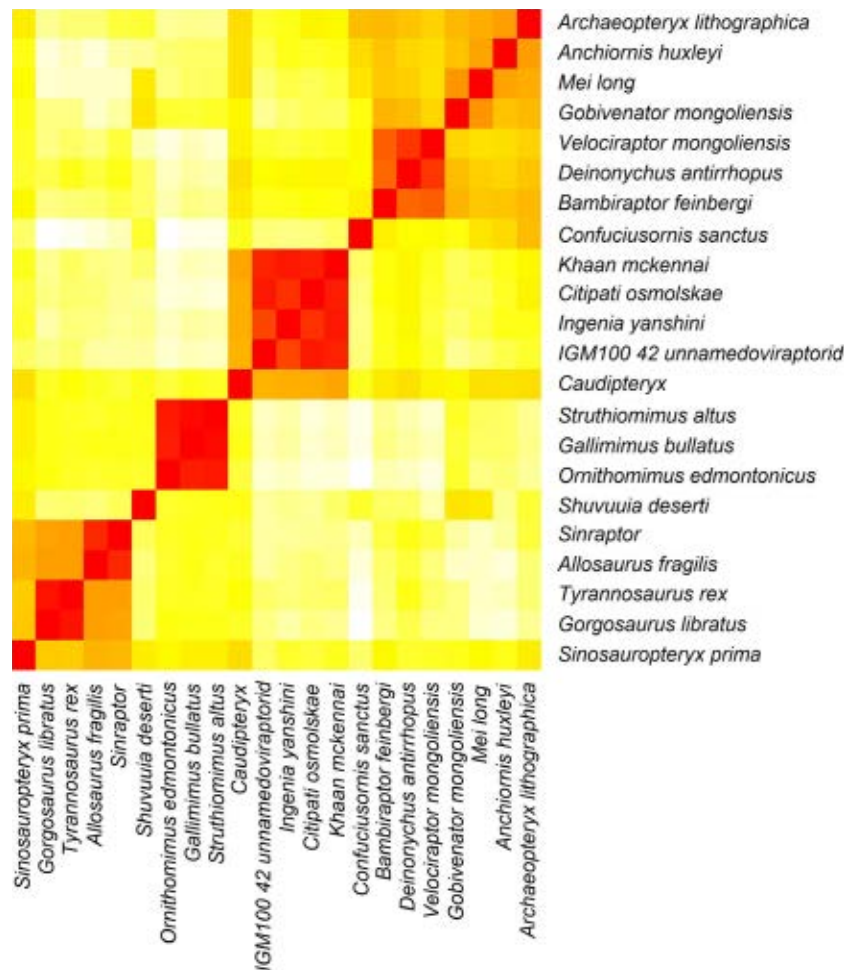
A Hopkins clustering measurement value above 0.5 corresponds to a data set which is acceptable for cluster analysis. A value above 0.75 denotes a good quality data set for such analysis.<sup>16</sup> Version 3.6.0. of R was used.<sup>17</sup> Cytoscape 3.7.2. was used to generate figure 6.

The BDIST algorithm was used for analysis of the Livezey and Zusi data set, available at [coresci.org/bdist.html](http://coresci.org/bdist.html).<sup>18,19</sup> A relevance cut-off of 0.95 was used in the analysis. The EntropyFilter.R R script was used, and is available at [github.com/csmaty/EntropyFilter2](https://github.com/csmaty/EntropyFilter2).

## Results

### Analysis of the Livezey and Zusi bird data set

To ensure accurate results with the data we are analyzing, we decided to run the algorithm on a data set, which can serve as a sort of gold standard. This data set contains morphological measurements of birds whose baraminic status is well known. Birds have been studied extensively in baraminology studies, and baraminologists can say with a high level of confidence which baramin(s) these birds belong to, for example that of Galliformes, or the ‘landfowl’ kind.<sup>20</sup>



**Figure 3.** Heat map of the proximity matrix from the BDIST results of the filtered van der Reest data set. Lighter colours represent proximity values close to 1, denoting species within the same baramin. Darker colours represent proximity values close to 0, denoting species from different baramins.

The validity of this kind has been supported by biblical evidence, hybridization data, and ortholog protein content.<sup>21</sup>

A morphological data set containing data for 2,954 characters for a wide variety of 188 bird species assembled by Livezey and Zusi<sup>22</sup> was analyzed. The BDIST software was used to analyze this data set using a relevance cut-off value of 0.95. The result can be seen in supplementary figure 1. The stress graph (supplementary figure 2) also shows minimal stress at only two dimensions. This result does an excellent job at illustrating the need to improve the BDIST algorithm with a better clustering method.

Thus, the data set was entropy filtered, using the Entropy Filter R script, described in the Materials and Methods section. A maximum ratio of undetermined values was set to 25% for both rows and columns. The minimum entropy value was set to 0.25. During this process, the percent of undetermined values dropped from 22.1% to 1.6%. The mean character entropy rose from 0.32 to 0.57. Of the 188 initial

**Table 2.** Difference in clustering using the BDIST method and hierarchical clustering for the entropy-filtered Brusatte data set

Species	BDIST cluster no.	Hierarchical cluster no.
<i>Albertosaurus sarcophagus</i>	1	1
<i>Alioramus</i>	1	1
<i>Daspletosaurus</i>	1	1
<i>Gorgosaurus libratus</i>	1	1
<i>Tarbosaurus baatar</i>	1	1
<i>Tyrannosaurus rex</i>	1	1
<i>Allosaurus fragilis</i>	2	2
<i>Dilong paradoxus</i>	2	2
<i>Guanlong</i>	2	2
<i>Sinraptor dongi</i>	2	2
<i>Archaeopteryx lithographi</i>	3	3
<i>Bambiraptor feinbergorum</i>	3	4
<i>Deinonychus antirrhopus</i>	3	4
<i>Velociraptor mongoliensis</i>	3	4
<i>Citipati osmolskae</i>	3	5
<i>Gallimimus bullatus</i>	4	6
<i>Sinornithomimus</i>	4	6
<i>Struthiomimus altus</i>	4	6
<i>Shuvuuia deserti</i>	3	7

**Table 3.** Statistics for the hierarchical clustering for the entropy-filtered Brusatte data set

baramin	species	min	mean	max	st. dev.	p-value
1 (tyrannosaurid1)	6	0.824	0.904	1	0.046	3.33E-21
2 (tyrannosaurid2)	4	0.743	0.811	0.973	0.098	1.00E-03
4 (dromaeosaurids)	3	0.959	0.973	0.986	0.014	1.17E-23
6 (Ornithomimidae)	3	0.932	0.955	0.973	0.021	1.98E-09

species, 147 (78%) remained, with 1,136 of the 2,954 characters (38.4%) also remaining, corresponding to a 3.3-fold data reduction. The filtered data set was then inputted into the BDIST algorithm. The results can be seen in supplementary figure 3: entropy filtering resulted in two larger and three smaller clusters. However, as can be seen in the stress graph in supplementary figure 4, there is minimal stress at 49 dimensions. Clearly, the clustering method must be improved.

Therefore, the distance matrix resulting from the BDIST analysis on the filtered data set was transformed into a proximity matrix according to the procedure outlined in Materials and Methods. Hierarchical clustering was applied to this matrix, which can be seen in the baraminic heatmap in figure 1.

In total, 70 putative clusters were discovered, among them many small groups, as can be seen in the baraminic heatmap. The species and cluster number for the 147 species can be found in supplementary file 1 online, seen in table 1. Overall, 16 statistically significant putative clusters were discovered using hierarchical clustering. These clusters correspond to several orders, superfamilies or families of birds. For example, the superfamily Galliformes was found in the analysis of the proximity data set.<sup>21</sup> Several groups within the Caprimulgiformes apobaramin also emerged. These include the families *Caprimulgus*+*Nyctibius*+*Podargus*. The genus *Steatornis* and *Aegotheles* formed their own cluster. In contrast with previous baraminology studies, *Podargus* didn't belong to the same cluster as *Steatornis*.<sup>23</sup> This may be due to the fact that a large number of species were taken from a large number of groups in this study.

The Brusatte data set

To assess the cluster tendency of our data sets, the Hopkins clustering statistic was used. For the proximity data set of the Brusatte results we calculated a



value of 0.871. This means that this data set can very well be used for cluster analysis. In the following, we will refer to groups of species found by our algorithm as clusters. Hypothetically, these clusters should correspond to baramins, but can only be labelled as such tentatively, until supported by further evidence.

Following this method, seven clusters were found. The proximity matrix is displayed in figure 2. Here we can see four larger clusters, and three singleton species, *Archaeopteryx lithographica*, *Citipati osmolskae*, and *Shuvuuia deserti*. Whereas in the previous analysis these three species were lumped together with the dromaeosaurids, they now stand separately.

Next, we compared how this clustering relates to the old analyses (table 2). As we can see, 14 of the 19 species (73.7%) were assigned to the same group. In table 3 the four largest clusters are listed with at least three members. These are tyrannosaurids 1 and 2, dromaeosaurids, and the family Ornithomimidae. The four largest clusters (ones with more than two members) have statistically significant p-values. The proximity matrix and the clusters and stats are available online in supplementary file 2.

The van der Reest data set

Next, we wanted to see how well we could reclassify species from the van der Reest data set. The Hopkins clustering statistic for the proximity matrix used for this data set was 0.746, which is fair quality for clustering, but somewhat worse than the Brusatte data set. Using hierarchical clustering revealed 10 clusters, which are presented as a proximity matrix (heatmap in figure 3). In the heatmap we can see four larger groups—species belonging to clusters 1, 3, 5, and 7 listed in supplementary data file 2. These four larger clusters also have statistically significant p-values.

**Table 4.** Difference in clustering using the BDIST method and hierarchical clustering for the entropy-filtered van der Reest data set

Species	BDIST cluster no.	Hierarchical cluster no.
<i>Allosaurus fragilis</i>	1	1
<i>Gorgosaurus libratus</i>	1	1
<i>Sinraptor</i>	1	1
<i>Tyrannosaurus rex</i>	1	1
<i>Anchiornis huxleyi</i>	2	2
<i>Archaeopteryx lithographica</i>	2	2
<i>Bambiraptor feinbergi</i>	2	3
<i>Deinonychus antirrhopus</i>	2	3
<i>Velociraptor mongoliensis</i>	2	3
<i>Caudipteryx</i>	3	4
<i>Citipati osmolskae</i>	3	5
<i>IGM100 42 unnamed oviraptorid</i>	3	5
<i>Ingenia yanshini</i>	3	5
<i>Khaan mckennai</i>	3	5
<i>Confuciusornis sanctus</i>	2	6
<i>Gallimimus bullatus</i>	4	7
<i>Ornithomimus edmontonicus</i>	4	7
<i>Struthiomimus altus</i>	4	7
<i>Gobivenator mongoliensis</i>	2	8
<i>Mei long</i>	2	8
<i>Shuvuuia deserti</i>	5	9
<i>Sinosauropteryx prima</i>	1	10

**Table 5.** Statistics for the hierarchical clustering for the entropy-filtered van der Reest data set

baramin	species	min	mean	max	st. dev.	p-value
1 (tyrannosaurid)	4	0.816	0.977	0.867	0.076	1.10E-4
3 (dromaeosaurid)	3	0.883	0.937	0.904	0.029	1.34E-4
5 (oviraptor)	4	0.922	0.968	0.954	0.019	8.23E-21
7 (ornithomimid)	3	0.964	0.987	0.973	0.012	1.12E-11

**Table 6.** Difference in clustering using the BDIST method and hierarchical clustering for the entropy-filtered Lamanna data set

Species	BDIST cluster no.	Hierarchical cluster no.
<i>Velociraptor mongoliensis</i>	1	1
<i>Herrerasaurus ischigualastensis</i>	1	2
<i>Citipati osmolskae</i>	2	3
<i>Conchoraptor gracilis</i>	2	3
<i>Ingenia yanshini</i>	2	3
<i>Khaan mckennai</i>	2	3
<i>Nemegtomaia barsboldi</i>	2	3
<i>Rinchenia mongoliensis</i>	2	3
<i>Yulong mini</i>	2	3
<i>Zamyn Khondt oviraptorid</i>	2	3
<i>Anzu wyliei</i>	3	4
<i>Archaeopteryx lithographica</i>	1	5
<i>Avimimus portentosus</i>	4	6
<i>Caudipteryx zoui</i>	5	6
<i>Incisivosaurus gauthieri</i>	5	6

**Table 7.** Statistics for the hierarchical clustering for the entropy-filtered Lamanna data set

baramin	species	min	mean	max	st. dev.	p-value
5 (oviraptor)	8	0.768	0.863	0.977	0.054	1.21E-29

Here also, we compared our new clustering patterns with those previously observed (table 4). Cluster statistics are presented in table 5. Ten out of 22 species (45.5%) classifications were the same in both the old and new analysis. The four largest clusters have statistically significant p-values at the 5% level. We found one of the same putative clusters as when we re-analyzed the Brusatte data set, a dromaeosaurid cluster and a new cluster of oviraptorids. However, in the re-analysis of this data set, we found that tyrannosaurids

form one large cluster instead of two clusters in the re-analysis of the Brusatte data set. This might be due to the selection of characteristics in the individual data sets.

The proximity matrix and the clusters and stats are available online in supplementary file 3 for this analysis.

The Lamanna data set

Lastly, we also re-analyzed the Lamanna data set. For this data set, the Hopkins clustering statistic was 0.739, which is fair clustering quality. Six clusters were determined. The proximity matrix is depicted in figure 4, showing one large cluster with eight species, together with either pairs of species or single species. The large cluster corresponds to an oviraptorid cluster, which was also found in the analysis of the van der Reest data set.

The old and new clustering can be seen in table 6. Twelve out of 15 classifications (80%) were shown to be the same in both the old and new analyses. Cluster statistics can be seen in table 7, showing that only one cluster with more than two members was determined, and has a statistically significant p-value. The proximity matrix and the clusters and stats are available online in supplementary file 4.

## Discussion

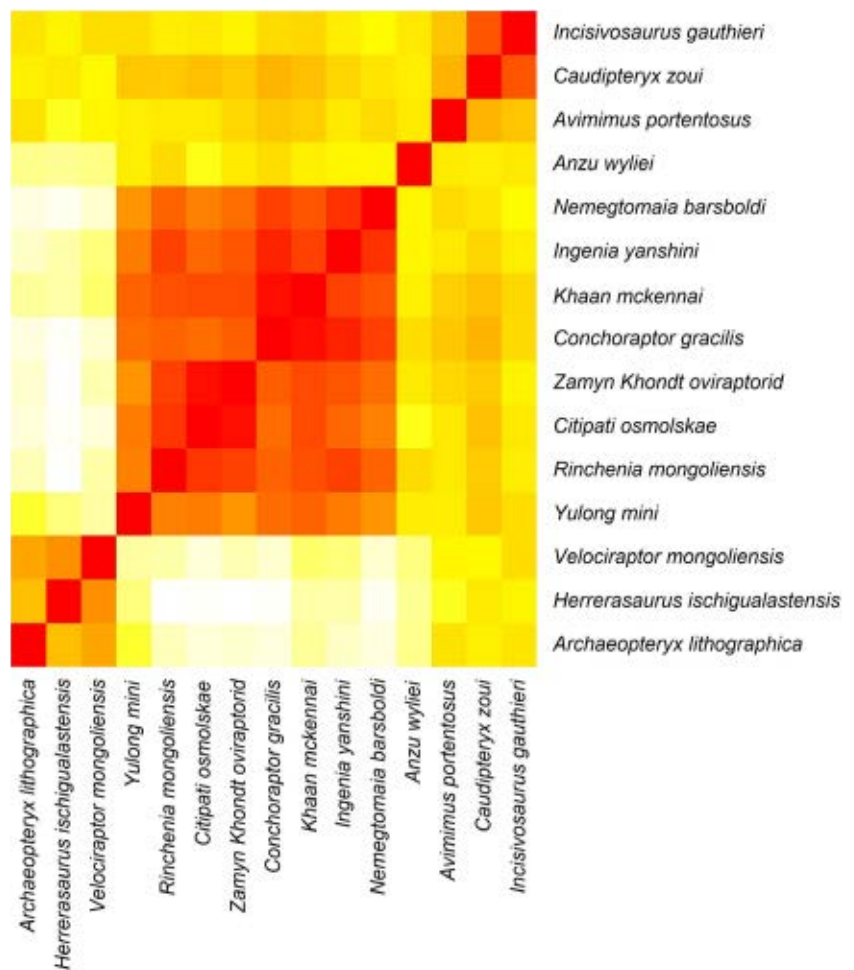
In our current study, we re-analyzed three dinosaur data sets from a previous analysis which employed entropy filtering, but which still gave obviously incorrect results (i.e. lumping *A. lithographica* together with dromaeosaurs). In order to correct these results, the BDIST pipeline was modified. Thus, a large-scale morphology data set for 188 bird species was entropy-filtered, used as input for the BDIST algorithm, and the resulting distance matrix was transformed into a proximity matrix, which was then subjected to hierarchical clustering. This method corrected the over-clustering, which was present in the BDIST results of both the initial, raw results as well as even the entropy-filtered BDIST results.

The present analysis succeeded in properly classifying the incorrect classifications coming from our previous analysis of the three dinosaur data sets. We observed a total of seven novel putative baraminic relationships based on the clustering we found in our results (depicted in figure 5). These are the tyrannosaurids (all species put together), dromaeosaurids, troodontid 1, oviraptor 1, theropod 2, ornithomimid, and *Archaeopteryx*, which includes *A. lithografica* and *A. huxleyi*.

In all three studies *A. lithografica* does not cluster with *Bambiraptor feinbergi*, *Deinonychus antirrhopus*, *Herrerasaurus ischigualastensis*, and *Velociraptor mongoliensis*. These dromaeosaurids consistently form a cluster in all three modified data sets. None of the latter four fossils have feather impressions or keratin signatures associated with them. Inferences based on *A. lithografica* anatomy strongly suggest that at the very least, it is a gliding bird, if not fully capable of flight. In particular, the classic defining bird trait is feathers, and *Archaeopteryx*'s asymmetrical feather impressions<sup>24</sup> and feather protein remnant signatures<sup>25</sup> are consistent with flight-capable remiges for the extinct creature.

However, the lack of a keel in *Archaeopteryx* implies a much smaller pectoralis major muscle than modern powered-flight birds such as the passerines. Why would a bird have feathers to fly but no muscles to power flight? From a creationist perspective it shows design features for gliding, not for flying. The modern roadrunner (*Geococcyx*) may approximate the form and function of *Archaeopteryx*. However, *Geococcyx* has no wing claws. Whereas *Geococcyx* uses terrain to elevate itself, perhaps *Archaeopteryx* used its wing claws and other features in more arboreal settings. Like roadrunners, once elevated, the bird could glide downward. This again supports the idea that certain characters should be given more weight than others. For example, with birds, the presence of feathers should have much more weight than the size of bones, which can be up- or down-scaled genetically.

In the van der Reest study, *A. lithografica* clustered together with *Anchiornis huxleyi*. Both of these species have a similar wing structure, with slender feather shafts, meaning they



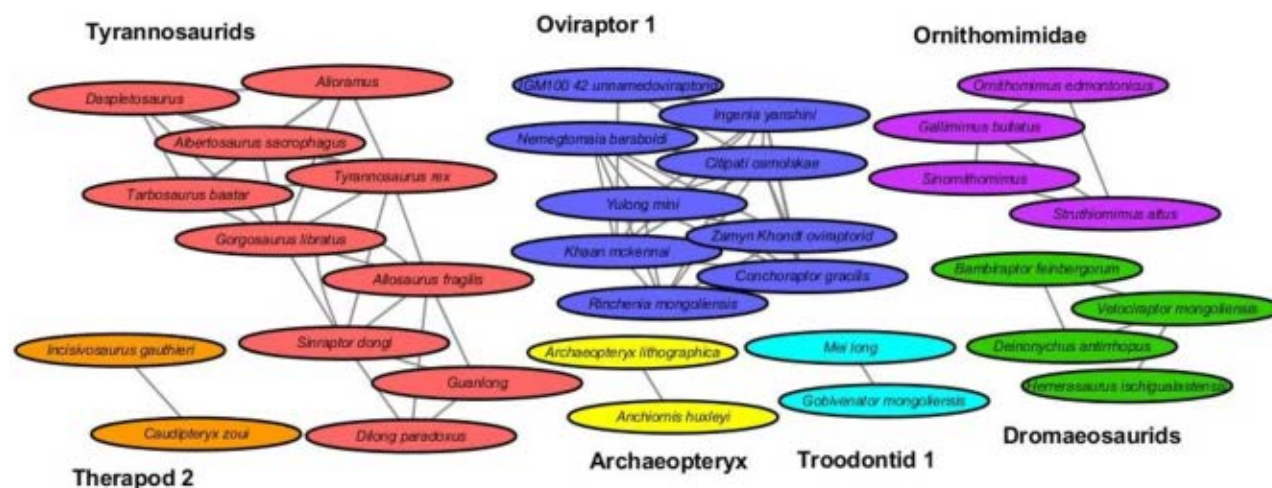
**Figure 4.** Heat map of the proximity matrix from the BDIST results of the filtered Lamanna data set. Lighter colours represent proximity values close to 1, denoting species within the same baramin. Darker colours represent proximity values close to 0, denoting species from different baramins.

had similar flight mechanisms.<sup>26</sup> In contrast, *Confuciusornis sanctus* has elongated primary feathers, with short covert feathers, resembling modern birds.<sup>27</sup>

Nine species all make up a larger cluster, throughout the three studies: *Citipati osmolskae*, *Conchoraptor gracilis*, IGM100-42 unnamed oviraptorid, *Ingenia yanshini*, *Khaan mckennai*, *Nemegtomaia barsboldi*, *Rinchenia mongoliensis*, *Yulong mini*, and *Zamyn Khondt*. All of these are oviraptors, which are theropod dinosaurs with shortened, toothless skulls.<sup>28–30</sup>

*Gallimimus bullatus*, *Ornithomimus edmontonicus*, *Sinornithomimus*, and *Struthiomimus altus* all cluster together. They are all members of the theropod family of dinosaurs called Ornithomimidae. *Mei long* and *Gobivenator mongoliensis* are both troodontids. *Anzu wyliei* and *Avimimus portentosus* belong to separate oviraptor baramins. *Caudipteryx zoui* and *Incisivosaurus gauthieri* are members of the same theropod cluster. However, feathered dinosaur





**Figure 5.** Baraminic relationships between seven baramins representing 34 species from the BDIST results of the combined Brusatte, van der Reest, and Lamanna data sets.

doubt Feduccia and colleagues treated *Caudipteryx* as a flightless bird, perhaps analogous to flightless cormorants of the Galápagos islands, on the basis of precise arrangement of flight feathers on its hand.<sup>31</sup> However feathered it was, its wings were too small for flight, but its robust legs showed possible adaptation to terrestrial habitats.<sup>32</sup> Jones *et al.* noted its anterior centre of mass resembled those of cursorial birds.<sup>33</sup> By grouping *Caudipteryx* among theropods, our modified BDIST method has not captured the separation of *Caudipteryx* as a bird and not a reptile. This is likely due to the similarities in gross morphology, if not in important details like feathers versus not feathers, between theropod and *Caudipteryx* anatomy.

*Shuvuuia deserti* and *Sinosauropteryx prima* are also theropods but belong to separate clusters. This result compares well with the assignment of *Sinosauropteryx* to the compsognathid dinosaurs particularly on the basis of papulose skin scale—not feather—preservation on its tail.<sup>34</sup> Chiappe also grouped *Compsognathus* with *Velociraptor* among theropods based on its cursorial anatomy and curved, serrated teeth that birds do not have.<sup>35</sup>

Lastly, there is a discrepancy between the way tyrannosaurids are classified according to the Brusatte and the van der Reest data sets. Whereas the re-analysis of the van der Reest data puts *Allosaurus fragilis* and *Sinraptor* into the same baramin as *Tyrannosaurus rex*, the Brusatte re-analysis puts them into a separate cluster, together with *Guanlong* and *Dilong paradoxus*. It could be that the two data sets were put together using different characters, or there may be more than one tyrannosaurid baramin. This is not uncommon, since previous baraminology studies have predicted multiple turtle and squid baramins.<sup>36,37</sup>

In contrast with the tyrannosaurids, this study successfully predicted the dromaeosaurid, oviraptor, and Ornithomimidae clusters in the re-analysis of the three data sets.

This means that the modified algorithm finds more consistent results than the BDIST method alone.

## Conclusion

Baraminology studies may sometimes give results that might intuitively seem incorrect. For example, in the previous analysis of three dinosaur data sets, *Archaeopteryx lithographica* was classified as a member of a terrestrial dinosaur baramin, when it has anatomy for flight. From the Bible, we know that birds were created on separate days than terrestrial dinosaurs, therefore they must belong to separate baramins. Feathers also provide a clear anatomical separation of Class Aves from Class Reptilia. Applying the extended entropy filter + the hierarchical clustering algorithm to the BDIST method corrected this. Furthermore, this method may be used as a possible tool in order to predict putative baramins more accurately.

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# Hierarchical clustering complicates baraminological analysis

Matthew Cserhati and Robert Carter

Baraminology is the study of the created kinds in Genesis 1. Its main goal is to determine the boundaries between each kind and the species membership within kinds. The science of baraminology has been developing for several decades. Besides morphology-based methods, multiple molecular baraminology studies have been performed using DNA and protein sequences. All these studies attempt to use some statistical measurement parameter to determine which species are close to one another, and thus may belong to the same kind, and which ones are not. There have been difficulties in determining a universal cut-off parameter that can be easily used to separate species into different kinds. One major issue is the hierarchical structure of species relationships. This makes it extremely difficult to know where to draw the line between kinds and prevents a simple statistical determinant. This paper examines this problem in the analysis of 28 mammalian species. Several possible ways forward in determining kinds are discussed.

Baraminology is the discipline of biblical taxonomy. Its main goal is to determine the species membership of the created kinds, called baramins, mentioned in Genesis 1, and to determine the boundaries between them. Species within the same kind should show continuity with one another on a morphological and a molecular level. They should also show discontinuity with all other species outside their kind. Over 10 years ago, Peer Terborg proposed a method to just do so based on genetic fingerprints in essential (i.e. non-redundant) genes. A handful, sometimes only one, of essential genes might suffice to tell one baramin from another. Terborg coined them “indicator genes”.<sup>1</sup> Other researchers have called them “taxonomically restricted” or “orphan” genes.<sup>2</sup> Indeed, modern humans, Neandertals, and Denisovans all share the same form of sialic acid in the sugar coating on their cells (N-acetylneuraminic acid, or Neu5Ac). All apes and most other mammals have a different sialic acid (N-glycolyneuraminic acid, or Neu5Gc). This is a profound difference that would, for example, prevent egg-sperm recognition, creating instant reproductive incompatibility.<sup>3</sup> This can be added to the list of other unique genes that separate humans (including Neandertals and Denisovans) from apes, like the *FOXP2*<sup>4</sup> gene and the structure of chromosome 2.<sup>5</sup> Yet, even though discontinuity can be found, the difficulty is in *quantifying* that discontinuity.

Cut-off values used in baraminology studies

Baraminology studies have traditionally attempted to use a statistical measurement with which they can separate species into their corresponding kinds. Morphology-based baraminology methods include the baraminic distance (BDIST) measurement.<sup>6</sup> Molecular baraminology methods include sequence alignment and identity matrix analysis, the GCM

(Gene Content Method),<sup>7</sup> and the WGKS (Whole Genome K-mer Signature) algorithm.<sup>8</sup>

BDIST is a widely used morphology-based baraminology method which measures a set of characters in a group of species using a data matrix.<sup>9</sup> It measures ‘baraminic’ distances between species based on the proportion of mismatched characters over all characters. The method determines relevant characters which are present in a minimum proportion of the studied species. This relevance cut-off has been arbitrarily set between 75 to 95% in various morphological baraminology studies. BDIST also uses bootstrapping to determine which correlations between taxa are robust. The minimum bootstrap value of 90% is also arbitrary.

In molecular baraminology studies, genetic distance/similarity can be determined in several ways. One can calculate overall percentage-wise genome similarity. This can be done for shorter sequences where aligning sequences, such as mitochondrial, plastid, or bacterial genomes is relatively straightforward. Several earlier baraminology studies have focused on this.<sup>10,11</sup> Another method used a popular DNA searching algorithm (BLAST) to probe similarities between chimpanzee and human genomes. This revealed much greater distances between the two than earlier studies had shown,<sup>12</sup> further putting to rest the ‘myth of 1%’.<sup>13</sup>

Another way is by calculating the proportion of the overlap of orthologous protein content and the total orthologous protein content between two species (orthologs are genes and their corresponding proteins that can be matched between species). This is described using the Jaccard Coefficient Value (JCV). The JCV is the defining step of the GCM, which has been used to study several groups of organisms, from Nucleocytoplasmic Large DNA Viruses (NCLDV),<sup>14</sup> Archaea,<sup>15</sup> fungi, and mammals.<sup>16</sup>



A third way to measure genetic similarity is to calculate the Pearson Correlation Coefficient (PCC) of the k-mer content between two species. This has been implemented in the WGKS, which has been run on algae,<sup>17</sup> insects,<sup>18</sup> and several groups of mammals, including bears, mustelids (minks and weasels), felids (cats), procyonids (raccoons), and mephitids (skunks).<sup>19</sup>

#### Complicating factors

A common problem in baraminology studies is determining the cut-off value, above which two species belong to the same baramin, and below which they belong to separate baramins. Both morphological and molecular baraminology studies have failed, as of yet, to define a precise cut-off value which can be of general use for determining baraminic membership. If one chooses a cut-off score that can delimit created kinds among one group of species, this does not automatically mean the same cut-off score can be used to separate kinds using a different set of species.

This may be due to several factors. One is the type of species being studied. Prokaryotes and eukaryotes have different gene structures. Bacteria contain many passenger genes besides the core genes found in their genomes, which may lower JCV, since passenger genes are usually not shared between species. Also, genes may be pleiotropic in their effects, so a relatively small number of genes may cause large phenotypic differences (i.e. large cognitive differences between chimps and humans). This would raise the JCV cut-off in the study of such species, meaning that two genetically similar species might belong to 'obviously' separate kinds. These considerations make the conclusions of all baraminology studies purely relative, dependent on intuition more than numbers.

Complicating the picture for both molecular and morphological baraminology studies is that God could have created several baramins which show some genetic similarity, but which are different overall morphologically. For example, an evolutionary study, based on the insertion of

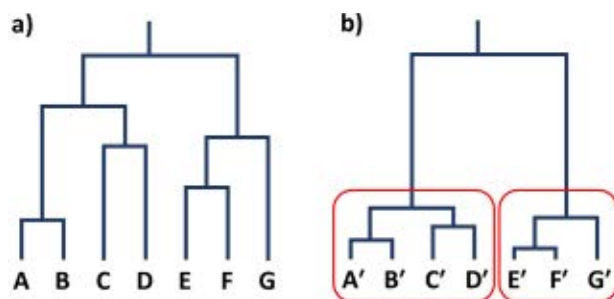
L1 retrotransposons alleges that Chiroptera (bats) and Perissodactyla (odd-toed ungulates, such as horses) are closer to one another than horses are to cows.<sup>20</sup> Yet another example is the overall relative genetic similarity between humans and the great apes. It is definitely possible that God could have created different kinds of organisms this way. We simply do not know what God had in mind when He created the living world.

When analyzing fossil data, researchers should strive to find the most complete data set possible. Incomplete fossil data sets make baraminic predictions very tentative. With more complete data, it is possible that these predictions may even change. For example, when first analyzing only craniodental characters in *Australopithecus sediba*, Wood classified this species as a member of the human holobaramin.<sup>21</sup> In a later analysis, including post-cranial data, he reversed his prediction, classifying *A. sediba* as an australopith.<sup>22</sup> One of the current authors initially placed *Homo naledi* in the human holobaramin, but then reassigned it as an australopith in a later study after including post-cranial features.<sup>23,24</sup> This highlights the difficulties inherent in the field. There is nothing wrong with these statistical analyses, but we need to always remember that the results are always tentative.

Gene-level similarities also occur. One example is the high sequence similarity between the oxygen-carrying protein hemoglobin in the blood of animals and the leghemoglobin protein, which fixes nitrogen in the root nodules of leguminous plants.<sup>25</sup> Another example is the *prestin* gene, which groups the bottlenose dolphin together with microbats.<sup>26</sup> Since genes with the same function and high sequential similarity are found in very different organisms, these genes can be viewed as functional design elements. But they complicate the baraminological landscape since they give the impression that very different baramins are actually similar to one another.

Another possibility is that, after the Fall, boundaries between kinds could have broken down. This does not seem to be true at this stage, but we cannot arbitrarily discount the possibility from first principles. Contrarily, genetic boundaries may have arisen which now block two species from breeding with one another, despite them belonging to the same original created kind at creation. Such mutations could involve chromosome incompatibilities, which make the hybrid offspring sterile, as in the (usual) case of the mule (63 chromosomes), which is the offspring of the horse (64 chromosomes) and the donkey (62 chromosomes). Such could also be the case with crypto-species, such as in several corals within the genus *Orbicella*, where incomplete gametic incompatibility exists, despite their belonging to the same genus, and hence most likely to the same created kind.<sup>27,28</sup>

Yet another thing to consider is that God could also have created multiple kinds, which seemingly belong to the same group, but are still separate from one another. For example,



**Figure 1.** a) Phylogenetic tree in which baramins are not clearly distinguishable. b) Phylogenetic tree in which species can be clearly divided into two putative clusters.

God could have created multiple turtle kinds,<sup>29</sup> seal kinds,<sup>30</sup> snake kinds,<sup>31</sup> or squid kinds.<sup>32</sup>

Finally, it is quite possible that massive gene loss, duplication, rearrangement, or genetic mutation and/or scrambling could create situations where statistics are unable to correctly identify baraminological relationships. This could easily be a contributing factor to why we have struggled to come up with an objective measure of intra-baraminic differences.

## Hierarchical relationships

Yet the greatest problem facing baraminology might well be the hierarchical structure of life. Even though God created organisms separate from one another, different kinds can still be placed into larger and larger groups, as in a hierarchy. For example, humans are primates, primates are mammals, mammals are tetrapods, tetrapods are vertebrates, vertebrates are deuterostomes, and deuterostomes are eukaryotes. As we ascend the hierarchy, organisms are classified less and less specifically.

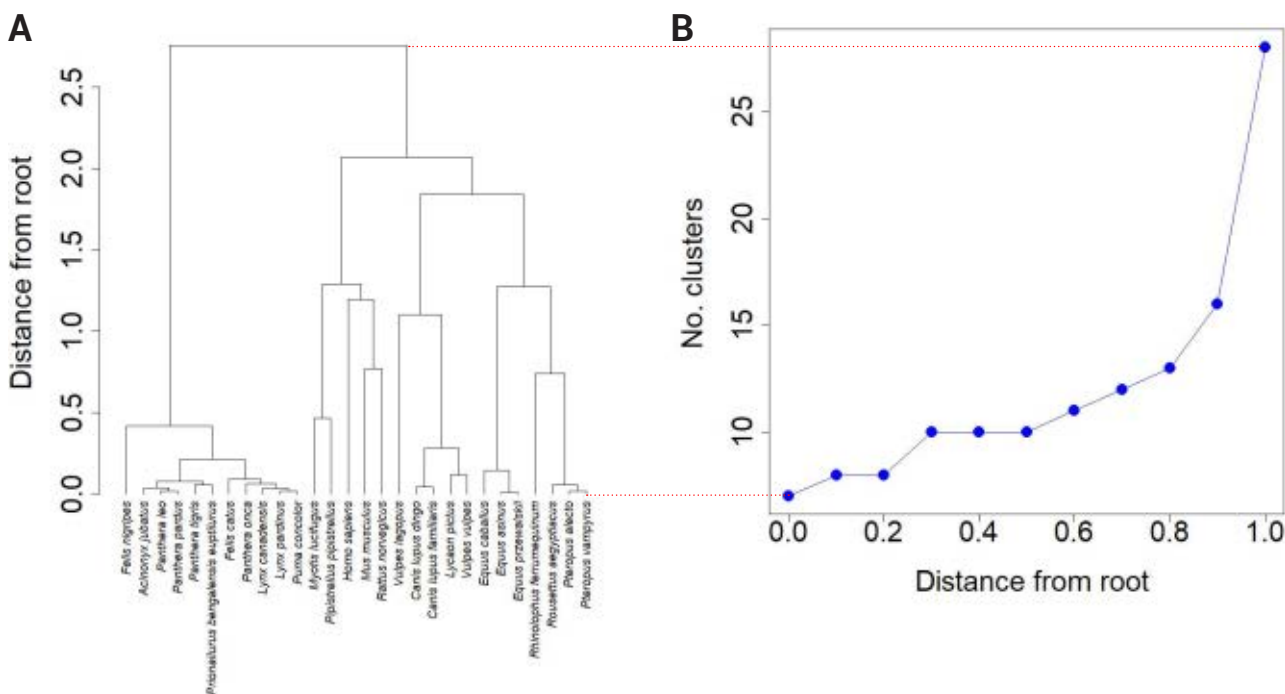
Another example is the vertebrate forelimb, which follows the same basic plan in all classes of vertebrates. The bones in the forelimb have a homologue in nearly all vertebrate classes with forelimbs. This has long been cited as evidence of common descent. Departing from the traditional evolutionary view, Wagner has recently argued that homology is an artefact of the evolution of gene regulatory networks.<sup>33</sup> ReMine argues that common traits within a hierarchy exhibit unity because of a common Designer and not common

descent.<sup>34</sup> Different created kinds differ from each other in the specific implementation of common design elements, such as differences in the order of limb bone development, origin of soft tissues, and differences in DNA codes.<sup>35</sup> Either way, similarity of design makes it harder to separate the kinds into distinct groups.

This simply means that cladistics can assemble any group of organisms into a hierarchy, regardless of whether they are truly related or not. And baraminology could be considered as just a mathematical expression of cladistics.

The biggest problem with hierarchical clustering is in deciding where to cut a cladistic/phylogenetic tree. In figure 1 we can see two extremes. In figure 1a, there is no clear clustering between species A–G. The tree looks like one big cluster. Species distances are uniformly distributed between 0 and 1. A high distance value would have to be used to get any kind of meaningful clustering. This is not optimal for baraminology studies.

In figure 1b, there is clear clustering. Here only a low distance value (corresponding to a high similarity value) is enough to distinguish between the two clusters. This kind of situation is optimal for baraminology studies. Yet, there was nothing preventing God from creating any particular pattern of similarity. Baraminology was designed to elucidate the real patterns, but it had no way of making absolute judgments about the boundaries between kinds. This became more obvious as variable levels of difference were discovered between groups of species belonging to what we thought were obviously distinct kinds.



**Figure 2.** A) Phylogenetic tree showing relationships between the 28 species in this study. B) The number of clusters varies depending on where a cut-off ('imaginary horizontal line') is placed at a certain distance from the root (top) of the tree shown in part A.

Figure 2 shows a cladogram connecting 28 species using WGKS. Where should one draw a horizontal line to determine the boundaries between baramins? If this line is set at the top of the cladogram and slowly moved downward, the number of clusters steadily increases. This increase is shown on the right, in figure 2B. The number of clusters rises exponentially as we transition from (assumed) created kinds to

post-Flood species. The inflection point might denote the optimal number of clusters, but this would be a matter of convention or convenience only, since we still don't know where the breaks between kinds are.

Hierarchical clustering problems also present themselves when selecting species for baraminology studies. Species must be chosen at the right taxonomic level. If species are chosen too broadly, different clustering algorithms could put different species together which don't belong to the same baramin.

Conversely, if species are chosen from one single baramin, the algorithms will still find clusters. This was demonstrated in a study with 25 species of dogs using BDIST. It found different groups of dogs based merely on their general size.<sup>36</sup> Another study based on genome-wide pairwise divergences and mitochondrial DNA analysis involving two species of ancient cave lions (*Panthera leo spelaea*), 12 historic lions (*Panthera leo melanochaita*), and six modern-day lions (*Panthera leo*) showed three separate lineages. The first lineage comprising ancient lions in Siberia and the Yukon, a second lineage in western and northern Africa and south-west Asia, and a third in central and southern Africa.<sup>37</sup> Nevertheless, these three lineages correspond to a monobaramin. The cat kind is known to encompass 38 species based on evidence from hybridization.<sup>38</sup> But if there are groups within groups, clearly determining the cut-off score is the single most critical factor in determining the boundaries between the created kinds.

The species relationships are very much like a fractal. The branching pattern on the tree of life appears similar at multiple scales. Thus, the promise of baraminology has not yet manifested itself. We do not yet have a way to make statistical determinations of group membership.

## Materials and Methods

Species from generally accepted created 'kinds' (which have been well studied, such as cats and dogs) were selected to determine whether they

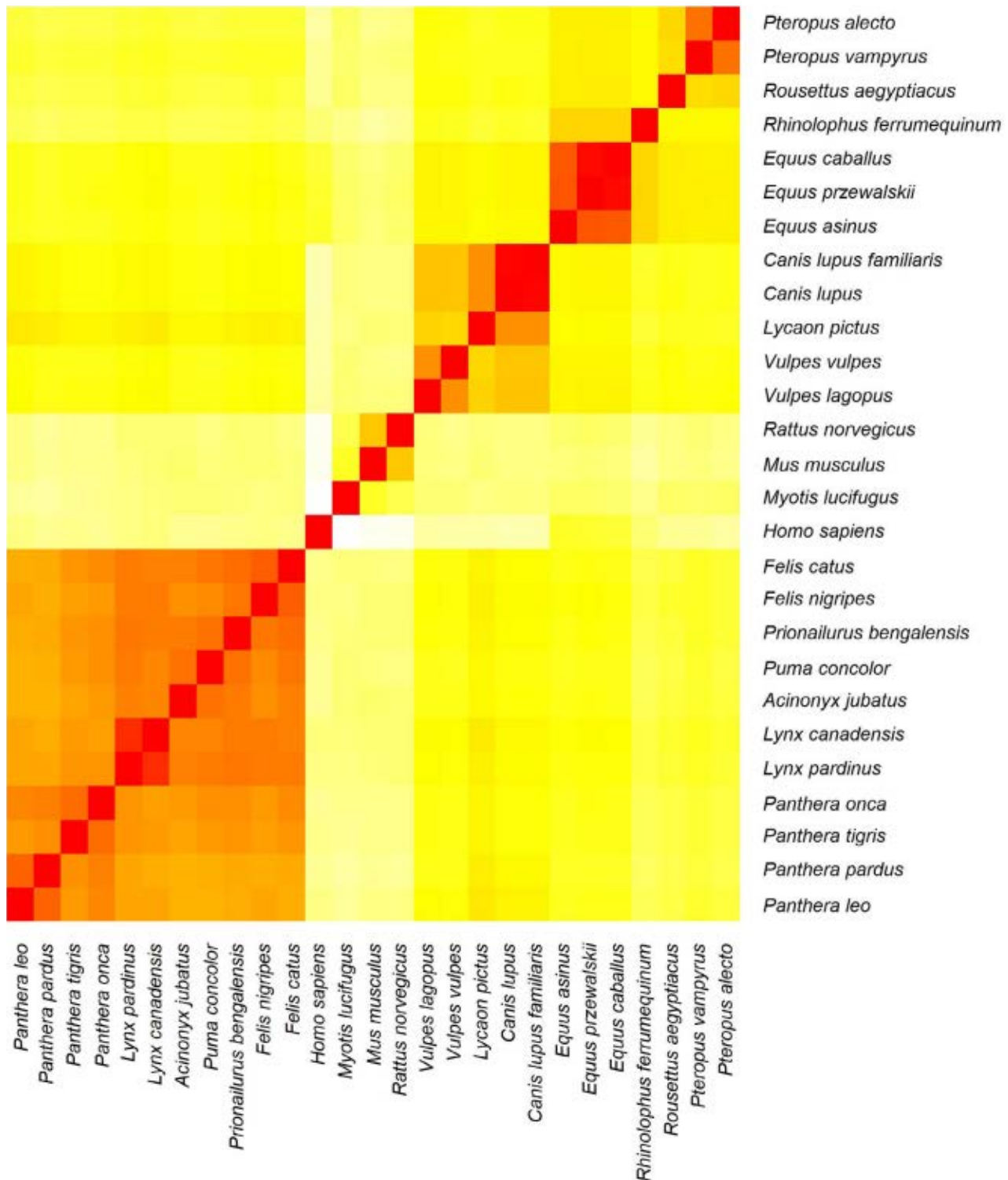
**Table 1.** Classification of the 28 species included in the mtDNA and WGKS analyses

Species	True cluster	mtDNA analysis	WGKS kmeans
<i>Acinonyx jubatus</i>	cat	cat 2	cat
<i>Canis lupus dingo</i>	dog	dog 1	dog
<i>Canis lupus familiaris</i>	dog	dog 1	dog
<i>Equus asinus</i>	horse	horse	horse
<i>Equus caballus</i>	horse	horse	horse
<i>Equus przewalskii</i>	horse	horse	horse
<i>Felis catus</i>	cat	cat 1	cat
<i>Felis nigripes</i>	cat	cat 1	cat
<i>Homo sapiens</i>	human	human	human
<i>Lycaon pictus</i>	dog	dog 1	dog
<i>Lynx canadensis</i>	cat	cat 1	cat
<i>Lynx pardinus</i>	cat	cat 1	cat
<i>Mus musculus</i>	mouse	mouse	mouse
<i>Myotis lucifugus</i>	microbat 1	mouse	microbat 1
<i>Panthera leo</i>	cat	cat 2	cat
<i>Panthera once</i>	cat	cat 2	cat
<i>Panthera pardus</i>	cat	cat 2	cat
<i>Panthera tigris</i>	cat	cat 2	cat
<i>Pipistrellus pipistrellus</i>	microbat 1	-	microbat 1
<i>Prionailurus bengalensis</i>	cat	cat 1	cat
<i>Pteropus alecto</i>	megabat	megabat	megabat
<i>Pteropus vampyrus</i>	megabat	megabat	megabat
<i>Puma concolor</i>	cat	cat 1	cat
<i>Rattus norvegicus</i>	mouse	mouse	mouse
<i>Rhinolophus ferrumequinum</i>	microbat 2	megabat	microbat 2
<i>Rousettus aegyptiacus</i>	megabat	megabat	megabat
<i>Vulpes lagopus</i>	dog	dog 2	dog 2
<i>Vulpes vulpes</i>	dog	dog 2	dog



really are members of these baramins. We used two methods to measure species similarity and dissimilarity, with a special focus on molecular baraminology methods. First, the

*Kalign alignment algorithm* was applied to a set of mitochondrial sequences belonging to 27 of the selected species. The alignments of the mitochondrial DNA are needed to



**Figure 3.** Heatmap of 27 species based on mtDNA sequence similarity. Higher species similarities between a given species pair correspond to redder colours. Lower similarity values correspond to yellow colours.

measure pairwise sequence similarity between all species. Second, WGKS was used to analyze the whole genomes of these baramins. These include the human, cat, dog, mouse, horse, and several putative bat kinds. The list of species, their genome sequence, and mitochondrial genomes are listed in Supplementary file part 1.

Mitochondrial genomes and whole genome sequences were downloaded from NCBI at [ncbi.nlm.nih.gov/genome](https://ncbi.nlm.nih.gov/genome). The *Kalign2* software program was used to align mitochondrial genomes on the EBI website at [ebi.ac.uk/Tools/msa/kalign](https://ebi.ac.uk/Tools/msa/kalign).<sup>39</sup> Pairwise whole genome sequence similarity was calculated and visualized in a heatmap in R, version 3.6.0, using the heatmap command under the ward.D2 clustering method. Previously established protocol was followed for WGKS, and pairwise Pearson Correlation Coefficient (PCC) values were visualized in a similar way.<sup>8</sup> Supplementary Files for this study are available at [creation.com/hierarchical-clustering-baraminology-analysis](https://creation.com/hierarchical-clustering-baraminology-analysis). The *kmeans* clustering algorithm was also applied, using the '*kmeans*' command to the PCC matrix with eight predicted clusters.

## Results

### Analysis of mitochondrial genomes

The identity matrix, which represents the percentage similarity between species, for the mitochondrial alignment is depicted as a heatmap in figure 3. The pairwise genome similarity values are available in Supplementary file part 2. The Hopkins clustering measurement value is 0.775, which means that the sequence similarity matrix has a reasonably good clustering quality. Seven groups are visible, these are the cat, dog, human, mouse, horse, and putative microbat and megabat kinds.<sup>40</sup> These groups are listed in column 2 of table 1. Using the *kmeans* clustering algorithm, the 27 species grouped together into eight clusters. The classification results are presented in column 3 of table 1.

### Analysis of whole genome sequences using WGKS

Next, we applied WGKS and tested for clustering performance. The Hopkins clustering value is 0.896, which indicates that the matrix is very good for clustering. The results are shown in figure 4. Statistical measures, such as the minimum, mean, maximum PCC value, standard deviation and p-value are provided in table 2.

*Kmeans* clustering was also applied to the PCC matrix, and nine clusters were predicted (see table 1, column 4). Supplementary file part 3 contains the PCC matrix as well as the clusters for each of the species in the WGKS analysis. Interestingly, *Homo sapiens* clusters separately from all other mammals, showing that it is indeed a unique species and forms its own kind. Its mean PCC with all other species is 0.226 ( $\pm 0.002$  SD), which is very low compared to all other kinds, again telling us humans are separate from all other species (Genesis 1:27).

The cat kind forms a distinct group, discontinuous from all other species. One species, *Felis nigripes* (black-footed cat) stands out from the other cats. Based on the mitochondrial DNA, the Y chromosome, the cytochrome b gene, and the 12S rRNA, some (evolutionary) researchers think that *F. nigripes* diverged early from all other cats.<sup>41,42</sup> This species is found in South Africa, Botswana, Namibia, and Zimbabwe, far from the initial post-Flood dispersal site of Ararat. This species has a mean PCC of 0.903 ( $\pm 0.012$  SD) with all other cat species from the cat kind, whereas the other cats have a mean PCC of 0.979 ( $\pm 0.012$  SD) among themselves.

In the dog kind, the Arctic fox (*Vulpes lagopus*) stands out from the four other dog species, with a mean PCC of 0.672 ( $\pm 0.014$  SD) compared with all other dog species, which have a mean PCC of 0.843 ( $\pm 0.149$  SD). Why the Arctic fox stands out is unclear, but as an arctic species it is highly adapted to a cold climate, demonstrated by a faster metabolism, specialized circulation, foot pads, and smaller/shorter extremities.<sup>43</sup>

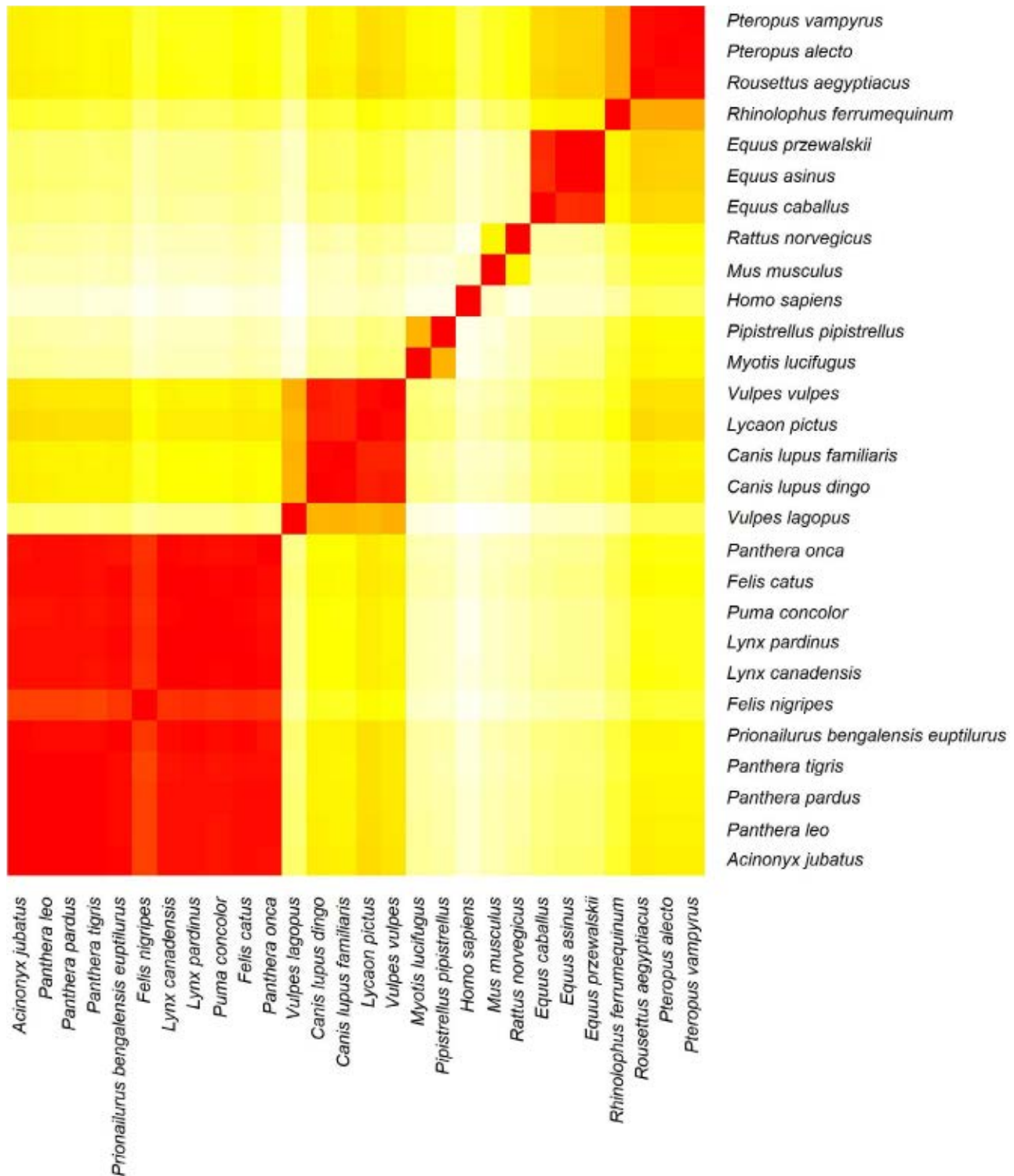
Mice and rats have a rather low PCC value of 0.463. However, a previous molecular baraminology study also grouped these two species into the same kind.<sup>16</sup>

**Table 2.** Statistical results for the WGKS algorithm on 28 mammal species

cluster	species	min	mean	max	stdev	p-value
cats	11	0.879	0.965	0.998	0.032	6.52E-162
dogs	4	0.939	0.957	0.985	0.020	1.76E-25
horses	3	0.924	0.950	0.995	0.039	9.34E-05
murids	2	0.463	0.463	0.463	NA	1.3E-27
vespertilionids	2	0.673	0.673	0.673	NA	3.26E-39
megabats	3	0.978	0.983	0.991	0.007	2.32E-40

Further, bats form three distinct groups, two of which are represented by the suborder *Microchiroptera* (microbats), and one by the suborder *Megachiroptera* (megabats). It is

unknown if they represent different kinds if separation and diversification occurred after the Flood among the bats. As with other animal species, God could have created multiple



**Figure 4.** Heatmap of 29 species based on WGKS similarity. Higher species similarities between a given species pair correspond to redder colours. Lower similarity values correspond to yellow colours.



bat baramins. In this case, some use echolocation, whereas others do not.<sup>44</sup> Echolocation is a complex trait, and so is not expected to vary within a kind, unless it is lost.

There are two main groups of microbats. These results mirror the results of a new molecular baraminology study which places *M. lucifugus* and *P. pipistrellus* into a tentative baramin, called Vespertilionoidea, and *R. ferrumequinum* into another tentative baramin, called Rhinolophoidea (see figure 4).<sup>45</sup> There is but one main grouping among the megabats. Two baraminology studies put megabats into their own baramin.<sup>45,46</sup> *Rousettus aegyptiacus* (Egyptian fruit bat), *Pteropus alecto* (black flying fox), and *Pteropus vampyrus* (large flying fox) cluster together within a megabat monobaramin (figure 4). *Pteropus* and *Rousettus* are both genera within the subfamily Pteropodinae, family Pteropodidae (flying foxes).

In figure 4, the three horse species (*Equus asinus*, *Equus caballus*, and *Equus przewalskii*) are found next to *R. ferrumequinum*. The three horse species show a very high mean PCC value of 0.950 ( $\pm 0.039$  SD). *E. asinus* and *E. caballus* have a PCC value of 0.924, *E. asinus* and *E. przewalskii* have a value of 0.995, and *E. caballus* and *E. przewalskii* have a PCC value of 0.932. Outside of their own kind, the three horse species have the highest average PCC values with the three megabat species (0.555–0.588,  $\pm 0.013$  SD), followed by the microbat *R. ferrumequinum* (0.469), see table 3. Interestingly, an evolutionary study based on L1 retrotransposon insertions concluded that *Chiroptera* (bats) and *Perissodactyla* (odd-toed ungulates, such as horses) form sister groups in the clade *Pegasoferae*, named after the mythical flying horse from Greek mythology.<sup>47</sup>

Nevertheless, *WGKS* accurately predicts these assumed baramins. Nine of the 27 species were misclassified by the mtDNA analysis (in bold in column 3 of table 1), corresponding to a classification efficiency of only 66.7%. In contrast, only one out of 28 species were misclassified by *WGKS* (for a clustering efficiency of 96.4%).

## Discussion

This study highlights one of the main problems of baraminology: the subjective classification of species into baramins.

The fact that life follows a hierarchical pattern makes it hard to delimit the created kinds. The thought that God frontloaded the created kinds with diversity-generating mechanisms<sup>1</sup> means that major changes to morphology, gene content, and gene sequence could have easily occurred within the creation model. Designed hemizyosity<sup>48</sup> could also lead to discordant gene content in the descendant species of any holobaramin. Even so, species are sometimes classified together into baramins based on intuitive considerations. While intuition may be a more subjective means of classifying organisms, it is still a part of science due to its inherent recognition of patterns. God created organisms and our goal as creation scientists is to think God's thoughts after Him. Adam, as the world's very first taxonomist was able to name the animals when God led them to him (Genesis 2:19–20), albeit with perfect, sinless mental capabilities. We may have to rely on a holistic, multi-lined approach to baraminic classification, including biblical, morphological, hybridization, and genetic data, as discussed in Ahlquist and Lightner (2019).<sup>49</sup>

Statistically speaking, a PCC value of  $> 0.7$  denotes a strong correlation between two vectors. This could possibly be used as a cut-off limit, but this remains to be evaluated. Another consideration is to use good quality datasets with good clustering statistics (i.e. Hopkins measurement  $> 0.75$ ). Or, the data can be pre-processed (i.e. normalization). Furthermore, apparent outliers may be excluded from the data set before clustering or noted as a small cluster. Post-clustering steps may also be taken to ensure quality results.<sup>39</sup> Several alternate statistical measures may indicate the presence of multiple clusters within a given data set. Testing for a Gaussian distribution in the distance/correlation measures can detect the presence of multiple clusters.<sup>50</sup> Different clusters may have different levels of distance values, each of which follows their own Gaussian distribution. Multiple modes (peaks of similarity) within the distribution are often important for discriminating groups. Applying principal component analysis to a non-Gaussian distribution can sometimes help to estimate the number of clusters.<sup>51,28</sup>

One possible way forward is to apply algorithms which automatically estimate the number of clusters within a

**Table 3.** PCC values between the horse species and several bat species

	<i>Equus asinus</i>	<i>Equus caballus</i>	<i>Equus przewalskii</i>
<i>Pteropus alecto</i>	0.581	0.555	0.582
<i>Pteropus vampyrus</i>	0.578	0.553	0.579
<i>Rousettus aegyptiacus</i>	0.588	0.563	0.588
<i>Rhinolophus ferrumequinum</i>	0.476	0.455	0.476

baraminology data set, instead of looking for a certain cut-off parameter. One such algorithm is the ‘gap statistic’ algorithm. This algorithm calculates the within-cluster sum of squares around the cluster mean for  $k$  clusters. The ‘optimal’ number of clusters can be thought of as the point after which the number of clusters does not decrease drastically.<sup>52</sup>

Another algorithmic procedure would involve estimating baramins by starting with the selection of a seed species. This seed species would represent a given baramin. Next, other species would be chosen which have the highest JCV/PCC values compared to the seed species. A mutually overlapping JCV value could be calculated for all species added to the seed species. The algorithm would stop adding species when either there is a statistically significant drop in the JCV values of the species added to the seed species.

This was done in the baraminology analysis of several halophilic species of Archaea. The results indicated that the difference in JCV between the three individual halophile species (*Halobacterium hubeiense*, *Halococcus salifodinae*, and *Halosimplex carlsbadense*) and their associated species were statistically significantly different than the JCV calculated for all other species (p-values: *H. hubeiense*: 2.4E-99; *H. salifodinae*: 1.9E-126; *H. carlsbadense*: 9E-115).<sup>15</sup>

Yet, this is similar to standard phylogenetic tree construction techniques, only using JCV instead of sequence data. Also, the algorithm could be tricked if it found a group of recently diverged species that, in turn, separated early from the parent baramin.

## Conclusions

The developing field of molecular baraminology is an exciting, yet challenging area of study within creation science. With further study we should be able to make useful progress. More than likely, a combined approach that uses morphological and molecular statistics, including orphan genes and hemizygous states, as well as a limited amount of user inference, will be needed.

## Glossary

**BDIST method:** a morphology-based baraminology method, based on comparing shared characteristics between a set of species.

**Cladistics:** a method of grouping organisms based on the proportion of characteristics that they have in common.

**Cryptospecies:** isolated populations of the same species which become incapable of mating with one another due to some genetic mutation.

**Deuterostome:** a large group of animals characterized by its embryonic development in which its first embryonic opening becomes the anus.

**GCM:** Gene Content Method, an algorithm, which determines baraminic membership based on the proportion of shared (orthologous) genes among species.

**Holobaramin:** the complete created kind, including all species pertaining to that kind.

**k-mer:** a segment of the DNA  $k$  bp long.

**Monobaramin:** a group of interrelated species that cluster together within a baramin.

**Orthologous protein:** a protein present in two species with a high degree of sequence similarity and which perform essentially the same function.

**Passenger gene:** genes which are not essential for an organism, and which were picked up from the environment, common in bacteria.

**PCC:** Pearson Correlation Coefficient, a statistical measure which tells us how similar two vectors are.

**Pleiotropic gene:** a gene with multiple effects in the phenotype.

**Tetrapod:** an animal with four limbs.

**Retrotransposon:** mobile genetic elements, which copy themselves into different parts of the genome, doing so through an RNA intermediate.

**WGKS method:** a molecular baraminology method which analyzes and compares the k-mer content of species within a study.

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# A biblical view restores reality to quantum mechanics

*D. Russell Humphreys*

The conventional view of quantum mechanics denies that particles have a definite position, momentum, and spin direction before those have been measured. A minority view (Appendix A) asserts that a particle always has definite values for those quantities, and that those 'hidden variables' influence the outcome of experiments measuring those quantities. Scripture appears to support the latter view. In the last few decades there have been many experiments trying to test which view is correct. They rely on a famous theorem by John Bell, called the Bell inequalities, to determine whether hidden variables exist or not. The conventional view violates the inequalities; Bell thought he proved that the minority view does not. Here I show that Bell's proof restricted the possibilities for hidden-variable theories and therefore does not apply to all such theories. I offer a counterexample, a hidden-variable model which gives the same correlation between widely separated detectors as orthodox quantum theory. This hidden-variable model violates Bell's inequalities, in just the same way as conventional quantum mechanics violates them. Recent experiments showing a violation of Bell's inequalities and conformity to standard quantum mechanics thus do not exclude the possibility of hidden variables. Therefore, the current alternative interpretation, 'entanglement' of particles, i.e. faster-than-light interaction between detectors, is not yet proven.

In 1928, Niels Bohr published<sup>1</sup> some of the ideas about quantum mechanics over which he and Einstein (figure 1) had their famous dispute at the 1927 Solvay conference in Brussels. Early in the paper Bohr wrote: "This [quantum] postulate implies a renunciation as regards the causal space-time coordination of atomic processes." Apparently, many theorists at the time took Bohr to mean that at least at the atomic scale, there can be no causal connection between two events with different spacetime coordinates. In particular, a particle could not have a definite trajectory between the points. He added: "Accordingly, an independent reality in the ordinary physical sense can neither be ascribed to the phenomena nor to the agencies of observation." In considering situations in which the specific orbit or trajectory of a particle is important, Bohr said: "we are bound to use the general solution of the wave equation which is obtained by superposition of characteristic solutions." Applying this to Heisenberg's newly published uncertainty principle, Bohr implied that, before measurement, a freely moving particle is generally in a mixture of quantum states and therefore would have no definite momentum or position. Of importance for later discussions, notice that this indefiniteness would also include the orientation of the particle's spin.

## Biblical insight on the issue

We might expect the Bible to have something to say about whether the particles God created each have a definite existence (including position and velocity), or not. One verse is: "And there is no creature hidden from His sight, but all

things are open and laid bare to the eyes of Him with whom we have to do" (Hebrews 4:13).

"All things" should include God's tiniest creations, the subatomic and subnuclear particles. For them to be seen would require them to have definite locations, I would think. Furthermore, Bohr's interpretation needs an observer to take note of a measurement before a particle can have a definite location or velocity. This verse says there is always an Observer who sees everything, even the smallest matter He created. Taken at face value, then, the Bible disagrees with Bohr's interpretation of reality. Similar thoughts may have prompted Einstein to say to Bohr at the 1927 conference: "God does not play dice [to determine the outcome of an experiment] with the universe!" Bohr reportedly replied: "Einstein, stop telling God what to do!" It would be interesting to hear what God might say on the matter, in addition to the verse above.

## The controversy continues

In 1935, Einstein, Podolsky, and Rosen (EPR) took issue in print<sup>2</sup> with Bohr's ideas. They considered the case of two particles which are emitted simultaneously in opposite directions by a source, and then are measured with detectors far enough apart to disallow any interaction between them. Using standard quantum theory, EPR showed that a measurement of the momentum of one particle allows us to predict the momentum of the other particle. Or, if one detector determines the location of one particle, then we can predict the location of the other. According to EPR's objective definition



Figure 1. Niels Bohr (left) and Albert Einstein (right), December 1925

of ‘reality,’ this predictability means that both particles have real (definite) momenta and positions before they are detected. That contradicts Bohr’s interpretation.

EPR did not comment directly on a related problem for Bohr, made clear by later authors: how could two detectors far enough apart not to interact nonetheless give correlated readings? J.S. Bell’s comments<sup>3</sup> on some of Einstein’s other writings about EPR indicate that Einstein thought the correlation between detectors would occur simply because each particle would maintain a definite trajectory (a definite momentum and position at every time) from source to detector, just as would be the case in classical mechanics.

In a letter to Einstein dated 7 June 1935, Erwin Schrödinger proposed the term ‘entanglement’ to describe the correlations between the two particles EPR described, and a few months later published a paper about it.<sup>4</sup> The term has come into wide use in recent decades. The idea today is that the wave functions of two particles can sometimes become tangled up with each other at the source. Then the joint wave function spreads out in all directions like a spherical cloud as the (non-located) particles move apart. When one particle materializes in a detector, the entangled wave function instantly transmits the information (faster than light) to the opposite detector and instructs the other particle to materialize there.

Shortly after that, Bohr replied<sup>5</sup> to the EPR paradox by suggesting that the very choice of apparatus at the detectors could somehow explain the correlation. Apparently, he was implying that if one chooses to measure momentum (or position) at one detector, one somehow gets a correlated momentum (or position) at the other detector. A half-century later, Bell found Bohr’s reply hard to understand and suggested that Bohr may have been simply rejecting (without proof) EPR’s premise of ‘no action at a distance.’<sup>6</sup>

In 1952 David Bohm introduced an interpretation of quantum theory using what he termed ‘hidden variables’.<sup>7</sup> He proposed that the quantum-mechanical wave function is a real field that would influence the motion of real particles, the



Figure 2. John Stewart Bell, FRS

particles having always a definite position, momentum, spin, and other characteristics. These quantities would be the hidden variables. In a companion paper,<sup>8</sup> he devoted a section to discussing the EPR *gedanken* (thought) experiment. Interestingly, Bohm did not appear to consider his hidden variables as explaining the correlations between the detectors. Instead he suggested the interaction occurs “instantaneously through the medium of the  $\psi$ -field [the wave function]”, which sounds like the present-day idea of entanglement.

In 1964, John Bell (figure 2) published an article<sup>9</sup> about the EPR paradox that has become famous. He asserted that hidden-variable quantum theories can have certain qualities that could be checked experimentally. (He had just previously found that attempts to prove hidden variables impossible, such as a famous theorem by John von Neumann, were flawed.)<sup>10</sup> Many experiments have been done since then to test the existence of hidden variables. They all depend on the theorem Bell derived, in particular on several mathematical inequalities based on the theorem. The inequalities test the statistical correlations between two detectors located far from each other. Bell thought that all hidden-variable theories would obey the inequalities. In contrast, standard quantum theory would violate the inequalities. A recent experiment,<sup>11</sup> apparently without experimental loopholes, shows that the statistical correlation of its detector readings violates the Bell inequalities, and agrees with orthodox quantum theory. If all hidden-variable theories must indeed obey the inequalities, then the experiment would exclude hidden variables as an explanation for the correlations between detectors. The only other possibility so far suggested is that somehow each detector instantaneously interacts with the other one to produce the correlations, i.e. entanglement.

### Bell’s Theorem

Bell used an example, shown in figure 3, like one given by Bohm and Aharonov.<sup>12</sup> It depicts ‘a pair of spin one-half particles [such as electrons or protons] formed somehow in

the singlet spin state [spins opposite each other] and moving freely in opposite directions.' The particles can pass through Stern-Gerlach magnets (see Appendix B), beyond which detectors register either spin-up or spin-down counts (labelled +1 or -1 respectively) along the magnet axes **a** and **b**, each of which is a unit vector in various possible directions in a plane normal to the line from source to detector. Bell explained that if **a** is aligned with **b**, both quantum theory and experiment have the two particles having opposite spins in the detectors.

Next, Bell labelled the detector results *A* and *B*, and assumed that they are determined completely by the magnet axes **a** and **b** and a set  $\lambda$  of hidden variables:

$$A(\mathbf{a}, \lambda) = \pm 1, B(\mathbf{b}, \lambda) = \pm 1 \quad (1, 2)$$

Bell said that some of the set of hidden variables could be in common with both particles, but others of the set could be unique to each particle/detector. Note that *A* and *B* are step functions, not able to have any values between +1 and -1. Then Bell defined a correlation function  $P(\mathbf{a}, \mathbf{b})$  (see Appendix C), which gives a number between +1 and -1 that tells how strongly the readings of detectors 1 and 2 should be related, depending on the relative orientations of **a** and **b**:

$$P(\mathbf{a}, \mathbf{b}) = \int \rho(\lambda) A(\mathbf{a}, \lambda) B(\mathbf{b}, \lambda) d\lambda, \quad (3)$$

saying ' $\rho(\lambda)$  is the probability distribution of  $\lambda$ .' Bell compares eq. (3) to the correlation function that orthodox quantum mechanics would predict for the singlet state (opposite spins):<sup>13</sup>

$$P(\mathbf{a}, \mathbf{b}) = \langle \sigma_1 \cdot \mathbf{a} \sigma_2 \cdot \mathbf{b} \rangle = -\mathbf{a} \cdot \mathbf{b} = -\cos \theta \quad (4)$$

In this expression only,  $\sigma_1$  and  $\sigma_2$  are the quantum-mechanical spin operators for particles 1 and 2, respectively, and  $\theta$  is the angle between **a** and **b**. Bell then goes on to show that there is no way we can arrange for *A* and *B* in eq. (3) to depend on the set of hidden variables  $\lambda$  in order to get the right-hand side of eq. (4). The underlying reason for this impossibility turns out to be that *A* and *B* are step functions. Bell concluded that there should be a difference between the experimentally measurable correlation functions for hidden-variable theories and orthodox quantum mechanics. He thought all hidden-variable theories should obey his inequalities, whereas standard quantum theory violates the inequalities.

### A hidden-variable model that is a counterexample

Bell thought his *ansatz* (initial assumption), equations (1, 2) with step functions, was a correct representation of all hidden-variable theories. I suggest that this does not cover all the possibilities for hidden variable theories. Below is a counterexample. It shows at least one hidden-variable model that gives a correlation function identical to that of orthodox quantum mechanics,  $P(\mathbf{a}, \mathbf{b}) = -\cos \theta$ . So the model would violate the Bell inequalities, just as standard quantum theory does.

Imagine that each of the two particles in figure 3 has a definite location, momentum, trajectory, and unit spin vector  $\sigma$  as projected onto the plane of its detector. The source produces opposite spins in the two particles. Each particle is accompanied by waves that make it impossible to measure all these things precisely and simultaneously. The spin of each particle remains oriented in a particular direction all along its trajectory.

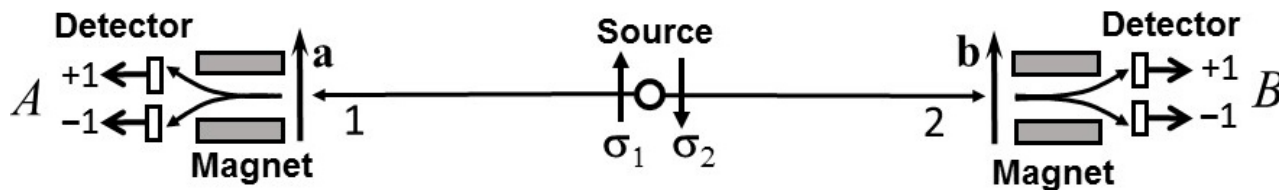
As figure 4 shows, the spin vector  $\sigma_1$  of particle 1 is at an angle of  $\lambda$  with respect to the Stern-Gerlach magnet axis (see Appendix B) for detector 1, vector **a**. The spin  $\sigma_2$  of particle 2 is at angle of  $\lambda + \pi + \theta$  with respect to the magnet axis of detector 2, vector **b**. Each emission of a particle pair from the source produces a specific value of  $\lambda$  which remains the same all the way to the detector, but over many events  $\lambda$  can have any value between 0 and  $2\pi$ . The correlation between detectors is produced by the source, with each particle retaining the spin information all along its path to the detector.

Here are the key differences I am introducing in this model. First, let us say that *A* and *B* are not step functions, but rather smoothly varying continuous functions whose *signs* give the reading (+1 or -1) of each detector:

$$\text{Reading of detector 1} = \text{sign}(A) \quad (5)$$

$$\text{Reading of detector 2} = \text{sign}(B) \quad (6)$$

(As Bell points out for a similar use of the sign function, the fact that the sign is undetermined for *A* or *B* being exactly zero makes no practical difference, since the probability of getting those exact values is zero). Using the sign function reflects the experimental observation that Stern-Gerlach magnets align the output spins with their axes, regardless of the initial spin directions of particles as they enter the magnets.



**Figure 3.** Bell's *gedanken* (thought) experiment has a source emitting two spin one-half particles (such as electrons or protons) in opposite directions. The spins,  $\sigma_1$  and  $\sigma_2$ , are opposite each other. The particles can pass through Stern-Gerlach magnets (see Appendix B) whose axes **a** and **b** can be oriented in any direction in planes perpendicular to the line between 1 and 2. The detector pairs remain lined up with the magnet axes. In Bell's analysis, *A* and *B* are step functions representing the outputs of the detectors, either +1 or -1.



That is, the output spins are either up or down with respect to the magnet axes. The amplitudes of  $A$  and  $B$  do not matter; they can be chosen for convenience. All the above replaces Bell's *ansatz*, equations (1, 2), with this one:

$$A(\mathbf{a}, \lambda, \alpha), B(\mathbf{b}, \lambda, \beta) \quad (7, 8)$$

The main difference is that  $A$  and  $B$  are now continuous functions. A minor difference is that I have broken out from the set  $\lambda$  two subsets,  $\alpha$  and  $\beta$ . These are the hidden variables that are unique to detectors 1 and 2, respectively. For example,  $\alpha$  and  $\beta$  might specify just where and how a particle enters each detector. The symbol  $\lambda$  now represents the subset (in this case a single parameter, namely spin) of the hidden variables that both particles have in common. That is,  $\lambda$  travels with the particles. Turning now to the correlation function of eq. (3), Appendix C derives the function  $\rho(\lambda)$  for this situation. It is:

$$\rho(\lambda) = \frac{1}{\pi} \quad (9)$$

This value for  $\rho(\lambda)$  turns out to normalize the correlation function, which we can now write in this form:

$$P(\mathbf{a}, \mathbf{b}) = \frac{1}{\pi} \int_0^{2\pi} d\lambda \overline{A(\mathbf{a}, \lambda, \alpha)} \overline{B(\mathbf{b}, \lambda, \beta)} \quad (10)$$

The bars represent averages over the variables  $\alpha$  or  $\beta$ , respectively. For this example of a hidden-variable dependence, I choose  $A$  and  $B$  to be such that the averages are:

$$\overline{A(\mathbf{a}, \lambda, \alpha)} = \boldsymbol{\sigma} \cdot \mathbf{a} \quad (11)$$

$$\overline{B(\mathbf{b}, \lambda, \beta)} = -\boldsymbol{\sigma} \cdot \mathbf{b} \quad (12)$$

This dot-product dependence is similar to that for fields in a polarized light beam transmitted through an analyzing filter. Figure 4 shows that the dot products in eqs. (11) and (12) depend on  $\lambda$  as follows:

$$\boldsymbol{\sigma} \cdot \mathbf{a} = \cos \lambda \quad (13)$$

$$\boldsymbol{\sigma} \cdot \mathbf{b} = \cos(\lambda + \theta) \quad (14)$$

Using eqs. (11) through (14) in eq. (10) gives:

$$P(\mathbf{a}, \mathbf{b}) = -\frac{1}{\pi} \int_0^{2\pi} \cos \lambda \cos(\lambda + \theta) d\lambda \quad (15)$$

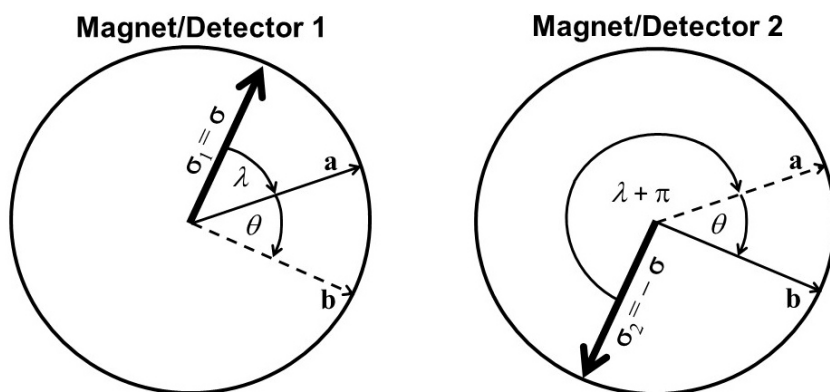


Figure 4. Orientations of spins ( $\sigma_1, \sigma_2$ ), and magnet axes ( $\mathbf{a}, \mathbf{b}$ )

Evaluating the integral<sup>14</sup> gives the correlation function for this hidden variable model:

$$P(\mathbf{a}, \mathbf{b}) = -\cos \theta \quad (16)$$

This is the same as the result from orthodox quantum theory, eq. (4). That means this hidden-variable model would violate the Bell inequalities in just the same way as orthodox quantum mechanics violates the inequalities.

## Conclusion

My counterexample shows that Bell's proof applies to only a subset of all possible hidden-variable theories. This means that experiments showing the correlation function has the orthodox form ( $-\cos \theta$ ) do not disprove the possibility of hidden variables. Thus we should not yet conclude that entanglement and instantaneous interaction are realities. It could be that correlations between detectors are merely due to information imparted at the source and preserved in transit to the detectors. In retrospect, that seems to be a much less extraordinary explanation than faster-than-light interaction between particles alleged to be entangled. After all, it is merely Bohr's *interpretation* (called the Copenhagen interpretation) of quantum data which suggested that an undetected particle has no specific trajectory and therefore can carry no information in flight. Einstein, of course, would be glad to hear that Bohr has not yet been validated by experiment. And if it is true that Bell originally hoped hidden variables would prove to be reality, he might have been glad to hear that his theorem has a loophole.

## Appendix A: The de Broglie-Bohm causal interpretation of quantum mechanics

Einstein never presented an explicit formulation of his idea that a particle should always have a definite position, momentum, and trajectory. One of the founders of quantum mechanics, Louis de Broglie, presented a paper with such a formulation at the 1927 Solvay conference. He called it the 'pilot-wave' theory, in which real waves would guide real particles. He later called it 'incomplete and diluted', and objections to it at the conference by Einstein and others caused him to set it aside. But he later returned to the theory, added much to it, and in 1960 published a book about it.<sup>15</sup> A little before that, David Bohm had published his work with similar ideas.<sup>16</sup> For the next three decades, a minority of physicists extended these ideas and collected them into a unified theory.<sup>17</sup>

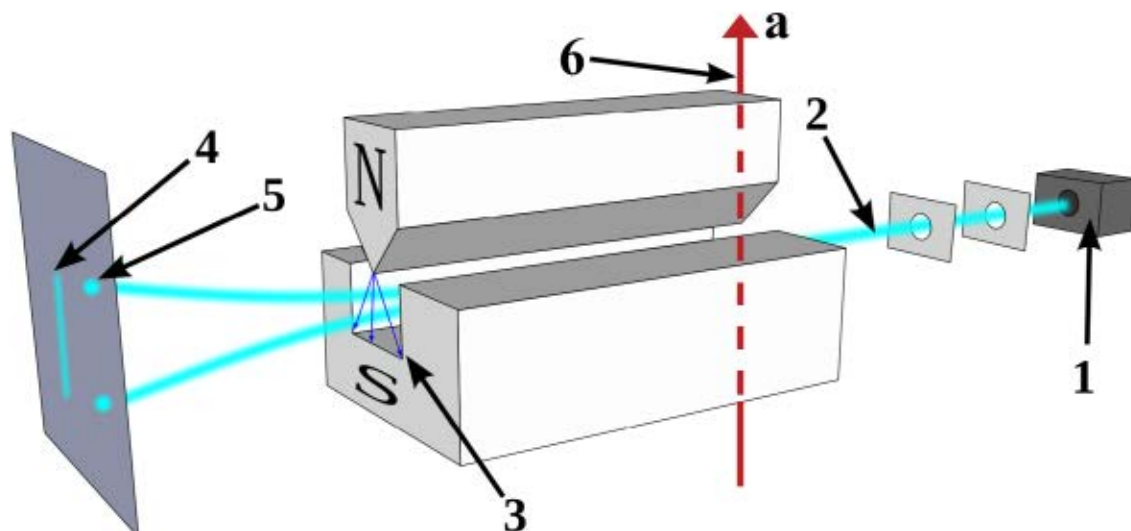


Image Tatoute, Wikimedia Commons/CC BY-SA 4.0

**Figure 5.** Stern–Gerlach experiment. Silver atoms travelling through a non-uniform magnetic field, and being deflected up or down depending on their spin: (1) furnace; (2) beam of silver atoms; (3) non-uniform magnetic field; (4) classically expected result; (5) observed result; (6) magnet axis, **a** (or **b**).

The basic idea is that particles always have a definite location and trajectory, and that they are accompanied by waves which are real, not mathematical constructs. (I add to the theory that the particles are the source of the waves.) The waves are able to influence the motion of the particles in a way that the theory specifies exactly. For example, in the famous ‘two-slit’ experiment, the particle goes through only one of the slits, but the waves go through both slits. Between the slits and the screen, the waves form an interference pattern. Depending on exactly where it goes through a slit, the particle will follow a path determined by the interference pattern. When it hits the screen, it contributes to an interference pattern on the screen that gradually becomes clear as more and more particles go through the slits. Theorists have plotted the sheaves of particle trajectories that result from the interference.<sup>18,19</sup>

### Appendix B: The Stern–Gerlach experiment

Figure 5 shows the essentials of a well-known experiment done in 1922 by Walther Stern and Otto Gerlach.<sup>20</sup>

A silver atom has one unpaired electron in its outer electron shell, so it has the spin and magnetism (like a tiny bar magnet) of a single electron. Before they enter the gap between the big bar magnets, the spins of the silver atoms are oriented randomly. When an atom enters the gap, the quantum-mechanical waves accompanying the atom force the main part of its spin to be aligned either up (with the field) or down (against the field). The non-uniformity of the field then pulls the spin-up atoms upward and pushes the spin-down atoms downward. So the silver beam splits into two parts as in item 5 of the figure. Without the quantum-mechanical waves, the spins of the atoms in the gap would

remain oriented randomly, and the beam would be a continuous sheet between up and down, as in item 4, the classically expected result. The magnet axis **a** (or **b**) in figure 3, figure 4, and the main text, is shown in item 6 of figure 5.

### Appendix C: The correlation function and $\rho(\lambda)$ for this case

From Bell’s writings, it was difficult for me to decide what exact form for the correlation function my model should use, in particular what numerical value I should use for his function  $\rho(\lambda)$  in eqs. (3) and (9). For example, he says: ‘Let the correlation function be defined as the mean value of the product  $AB$ .’<sup>21</sup> Is there not an already agreed-upon definition? Then in the following equation he does not show  $\rho(\lambda)$  at all. Is it 1, or is it subsumed in the averaging operation? So I decided to go for help to the branch of mathematics that developed the correlation function. Statistics textbooks define the correlation (in earlier texts called the ‘correlation coefficient’ and in this paper labelled  $P$ ) between two variables  $x$  and  $y$  as:<sup>22</sup>

$$P(x,y) = \frac{1}{n-1} \sum \left( \frac{x_i - \bar{x}}{s_x} \right) \left( \frac{y_i - \bar{y}}{s_y} \right) \quad (C1)$$

All the summations  $\Sigma$  here are for  $i=1$  to  $n$ . The values  $x_i$  and  $y_i$  are the  $i^{\text{th}}$  measurements of  $x$  and  $y$  in a set of  $n$  such measurements,  $\bar{x}$  and  $\bar{y}$  are the means of  $x_i$  and  $y_i$ , and  $s_x$  and  $s_y$  are the standard deviations of  $x_i$  and  $y_i$ . For  $x$ , the standard deviation is:<sup>23</sup>

$$s_x = \sqrt{\frac{1}{n-1} \sum (x_i - \bar{x})^2}, \quad (C2)$$

and similarly for  $y$ . For my case below, it turns out that the means  $\bar{x}$  and  $\bar{y}$  are zero. Using those values and eq. (C2) applied to both  $x$  and  $y$  in eq. (C1) gives:

$$P(x,y) = \frac{\sum x_i y_i}{\sqrt{\sum x_i^2 \sum y_i^2}}, \quad (C3)$$

The factors  $1/(n-1)$  all cancel out. Now use eqs. (11) – (14) to substitute the variables of my model for  $x$  and  $y$ :

$$x = \overline{A(a, \lambda, \alpha)} = \cos \lambda, \quad (C4)$$

$$y = \overline{B(b, \lambda, \beta)} = -\cos(\lambda + \theta) \quad (C5)$$

Now let us specify  $n$  values of  $\lambda$  in order from 0 to  $2\pi$  and call them  $\lambda_i$ . They are spaced a small angle  $\Delta\lambda$  from each other, and we have  $\Delta\lambda = 2\pi/n$ . That gives us  $n$  values of  $x$  and  $y$ :

$$x_i = \cos \lambda_i, \quad y_i = -\cos(\lambda_i + \theta) \quad (C6, C7)$$

Notice that the means of  $x_i$  and  $y_i$  are zero, as I said below eq. (C2). Put eqs. (C6) and (C7) into eq. (C3), and multiply all the sums by  $\Delta\lambda$  (keeping the ratio the same), to get:

$$P(x,y) = \frac{-\sum \cos \lambda_i \cos(\lambda_i + \theta) \Delta\lambda}{\sqrt{\sum \cos^2 \lambda_i \Delta\lambda \sum \cos^2(\lambda_i + \theta) \Delta\lambda}}, \quad (C8)$$

Now take the limit of each sum as  $\Delta\lambda \rightarrow 0$  and  $n \rightarrow \infty$ . That changes each sum to a definite integral:

$$P(a,b) = \frac{-\int_0^{2\pi} \cos \lambda \cos(\lambda + \theta) d\lambda}{\sqrt{\int_0^{2\pi} \cos^2 \lambda d\lambda \int_0^{2\pi} \cos^2(\lambda + \theta) d\lambda}} \quad (C9)$$

I have replaced  $x$  and  $y$  with  $a$  and  $b$  because  $\lambda$ ,  $\alpha$ , and  $\beta$  are integrated out of the result. Evaluating the two integrals in the denominator yields  $\pi$  for each one. That makes eq. (C9) become:

$$P(a,b) = -\frac{1}{\pi} \int_0^{2\pi} \cos \lambda \cos(\lambda + \theta) d\lambda \quad (C10)$$

This is identical to eq(15) in the main text, thus confirming eq. (9):

$$\rho(\lambda) = \frac{1}{\pi} \quad (C11)$$

This result contradicts Bell's assumption that  $\rho(\lambda)$  should be 'the probability distribution of  $\lambda$ ,' for in that case  $\rho$  would be  $1/2\pi$ . Instead, the statistical definition of the correlation, eq. (C1), shows that  $\rho$  is:

$$\rho = 1/(s_A s_B), \quad (C12)$$

where  $s_A$  and  $s_B$  are the standard deviations of the distributions  $A$  and  $B$ . For Bell's choice of step functions for  $A$  and  $B$ , this would still give  $\rho = 1/2\pi$ . But for my choice of  $A$  and  $B$  in eqs. (11) and (12),  $\rho$  is  $1/\pi$ .

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# The surprisingly complex tRNA subsystem: part 1 – generation and maturation

Royal Truman

tRNAs serve as linker molecules to translate mRNA sequences into protein sequences, but these require extensive processing by preexisting protein-based molecular machines. 5' leader sequences and 3' extensions must be removed using complex ribonucleases having virtually no similarity across prokaryotes, mitochondria, and eukaryotes. In plants, RNase P is a protein-only enzyme. Introns must also be removed but the location of the splice junctions differ for eukaryotes and archaea.

Aminoacylation occurs on the trinucleotide motif 'CCA' as a free RNA end on all tRNAs, a motif necessary for processing in ribosomes. tRNA genes encode the CCA sequence in *E. coli* and related bacteria, Gram-positive *Bacillus subtilis*, and some related bacteria. However, in nearly all eukaryotes and archaea the CCA sequence is not encoded and must be added post-transcriptionally.

All cells examined also encode an enzyme to repair the CCA sequence if damaged. The enzyme can discriminate against damaged tRNAs, causing defective ones to be degraded. A second quality control process found in all three kingdoms of life involves adding a second CCA to defective tRNAs as a degradation tag.

These observations support the view that cells could not have arisen without an overall plan.

The cellular genetic system is irreducibly complex, being composed of several collaborating sub-systems based on DNA, RNA, and proteins. Remarkably, the individual subsystems themselves, like mRNA (messenger RNA), DNA, ribosomes, and so on cannot exist independently without one or more of the others (figure 1). There is no simple evolutionary starting point. One could reason that since all organisms depend on DNA, perhaps this polymer was present first.

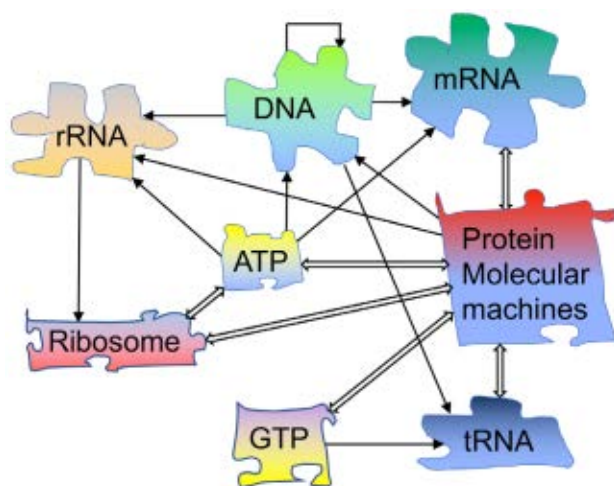
DNA, however, consists of nucleotides manufactured from pre-existing enzymes (protein-based molecular machines), and a new DNA strand requires a former one to already exist to serve as a sequence template. DNA replication requires many additional molecular machines such as polymerases, helicases, and topoisomerases. All these molecular machines are only produced by translating pre-existing mRNA (which comes from DNA) on pre-existing ribosomes. But the RNA and protein sequences used by ribosomes are themselves coded for on DNA.

Ever more circular dependencies are identified the deeper one looks. Transcription of portions of DNA to produce mRNA requires that RNA polymerases already exist, and translation only works if suitable tRNAs are already available (derived from DNA) and charged by aaRS (aminoacyl tRNA synthetases) which are additional molecular machines. This charging is not accurate enough without proofreading enzymes (yet more molecular machines). And none of the systems mentioned work without energy-supplying ATP or GTP molecules (created by complex machines requiring dozens of proteins). Everything requires something else.

It seems natural to conclude that an initial top-down design was necessary and then everything set up correctly. But this common-sense thinking contradicts the dominant naturalist paradigm. No form of intelligent planning nor contribution can be considered. But the deeper the subsystems themselves are examined the more dependencies are discovered. This is a dilemma. Evolution cannot work without enough minimal functionality to ensure survivability.

Documenting all the additional interdependencies in the genetic system seemed overwhelming, so we'll focus on the simplest subsystem for now: merely producing a collection of suitable tRNAs to serve as adaptor molecules needed to translate codons to the intended amino acid at ribosomes. Genetic code translation cannot occur without tRNAs, so they must have been present initially. To simplify, we will not consider the need for aminoacyl-tRNA synthetases, nor the proteins tRNAs need to interact with at ribosomes. These are separate subsystems which will require additional series of papers. We will even neglect details such as how Stop codons are recognized without requiring their own tRNAs.<sup>1,2</sup>

Parts 1 and 2<sup>3</sup> of this series cover processing of tRNAs, and chemical modifications for generating functional tRNAs, respectively. Part 3<sup>4</sup> covers additional quality control measures, and part 4<sup>5</sup> how customized RNA fragments derived from tRNAs are used for signalling and regulatory purposes. Finally, in part 5<sup>6</sup> we examine mathematically why there can be no simple starting point for the tRNA portion of the genetic code, and why evolution is incapable of developing stepwise the numerous complex processes that utilize tRNAs.



**Figure 1.** The cellular genetic system is composed of several mutually dependent subsystems. Single and double arrows represent an immediate, direct dependency for a particular subsystem to function. Dozens of protein-based molecular machines are indispensable such as DNA and RNA polymerases; topoisomerases; helicases (for nucleotide, amino acid and cell membrane synthesis); transcription factors; error correcting enzymes; aminoacyl tRNA synthetases, etc.

#### Overview and general information on tRNAs

The single-cell eukaryote yeast contains approximately 3 million tRNA molecules and the bacterium *E. coli* about 200,000.<sup>7</sup> tRNA is present in tens of millions of copies in a human cell and is the most abundant kind of RNA.<sup>8</sup> tRNA genes are found on mitochondrial and nuclear chromosomes, and nuclear-originating tRNA transcripts can be imported into mitochondria.<sup>8</sup> High tRNA gene sequence diversity is found in all mammalian genomes. Even the simplest eukaryote *Saccharomyces cerevisiae* has about 272 tRNA genes comprising 53 unique DNA sequences.<sup>8,9</sup>

Abundance, chemical modification, and charging levels (covalent attachment of amino acid to a tRNA in a high-energy state) are regulated to ensure proper decoding of mRNA in different cell types and cell states in environment-dependent ways. Translation is most active during the cell cycle when the cell doubles its protein mass before fission. During this time, the amount of tRNA increases, the relative proportion of *isoacceptors*<sup>10</sup> (tRNAs charged with the same amino acid but having different anticodons) change, most tRNAs get charged with activated amino acid, and chemical modification levels for most tRNAs are high.

When cells are stressed or cycle progression is halted, the major protein synthetic activity switches to stress response and other regulatory proteins.<sup>8</sup>

Spatial and chemical features of tRNAs must serve as informational signals to guide interactions with various components related to the translation apparatus. As an example, dozens to hundreds of different tRNA molecules must differ sufficiently in a cell so that the correct one can be reliably

aminoacylated by synthetases with the right amino acid.<sup>9</sup> This includes the tRNAs having different primary structures which must recognize synonymous codons (i.e. representing the same amino acid).<sup>11</sup>

In spite of considerable sequence variation, all cellular tRNAs must fold into almost identical three-dimensional structures to fit the relatively narrow tRNA binding sites of the ribosome during translation elongation. The folded cloverleaf secondary structure (figure 2) of every kind of tRNA requires Watson–Crick or wobble pairs in the four helical stems to produce a consistent structure. There are always either four or five inverted repeats that are responsible for formation of the stem-loop.<sup>12</sup> The structure must also optimize the specificity of codon-anticodon interactions between mRNA and tRNA.<sup>11</sup> Therefore, many chemical modifications are necessary to change the biophysical properties of the individual tRNAs before they can be used,<sup>13</sup> as we will discuss in part 2.

Genes encoding tRNAs for some anticodons appear in dozens of copies in individual organisms, while others are universally absent. This variability reflects the fact that mature tRNAs and degradation fragments derived from them regulate many cellular processes including protein expression level, translation accuracy, adequacy of protein folding, and even mRNA stability,<sup>14</sup> details we will discuss here and in part 2<sup>3</sup> and part 3<sup>4</sup> of this series.

Obtaining tRNAs from DNA is not a trivial matter and informational patterns are involved to demarcate the genes. Computer algorithms have been designed to identify tRNA genes using features such as the presence of highly conserved residues located at predictable distances from each other. This revealed at least 610 tRNA genes in the reference human genome.<sup>8</sup> Of these, 423 appear able to produce a stable tRNA structure, having 264 different DNA sequences.<sup>8</sup> The eukaryote tRNA genes are also preferentially localized in the nucleolus along with RNase P (discussed below), to facilitate mass production,<sup>9</sup> whereby RNase P seems to associate directly with the Pol III transcription apparatus through interactions with the transcription factor TFIIIB, which binds upstream of tRNA genes.<sup>9</sup>

#### I. tRNA gene variety

Scan-SE is a widely used bioinformatic tool to predict tRNA genes, based on predicted clover leaf secondary structure produced, sequence similarities across organisms, and various diagnostic intragenic tRNA promoter sequences.<sup>8,15</sup> Tools like these can produce false positives, but nevertheless as of 2014 approximately 600,000 tRNA genes were registered on the tRNA gene database.<sup>16</sup> The number of tRNA genes vary considerably across organisms, with the *Plasmodium falciparum*<sup>17</sup> parasite containing the lowest number of tRNA genes known for a eukaryotic cell (a total

of 46 nuclear genes encoding 45 tRNA isoacceptors). Two different genes encode the initiator and elongator tRNA<sup>Met</sup>.<sup>18</sup>

*Isodecoders* (tRNAs with different body sequences but the same anticodon).<sup>19</sup> Isodecoder expression varies widely in human tissues and is similar across mammalian genomes. The many isodecoders must carefully avoid being mischarged by the 19 other tRNA synthetases and therefore include hindering features for quality control purposes.<sup>8</sup> That so many similar isodecoders are present across many kinds of organism implies their dedicated use for comparable biological purposes.

Each isodecoder tRNA set is generated from a pool of tRNA genes. For example, 35 genes code for tRNA<sup>Ala</sup>(AGC) in the human genome.<sup>20</sup> Isodecoders have differential, tissue-specific functions. The five tRNA<sup>Arg</sup>(UCU) genes recognize the AGA codon of arginine. One of them (Tr-20) is very different in both sequences and the presence of introns. Tr-20 is primarily expressed in the central nervous system where it accounts for ~60% of all tRNA<sup>Arg</sup>(UCU) expression. One mutation which significantly reduces the expression of Tr-20 isodecoder increases ribosome pausing specifically at AGA codons and results in neurodegeneration, likely due to increased protein misfolding or degradation.<sup>8</sup>

*Isoacceptors.*<sup>10</sup> Since different codons can represent the same amino acid (i.e. synonymous codons) it is not necessary to have tRNAs with all  $4 \times 4 \times 4 = 64$  possible trinucleotide anticodon patterns if the system is properly designed. And indeed, in humans, tRNA isoacceptors are used to translate 12 amino acids: two for Glu, Lys, Gln; three for Ile, Val, Thr, Ala, Gly, Pro; four for Ser; and, five for Leu, Arg. For the six amino acids that are represented by only two codons each (Phe, Tyr, His, Asn, Asp, Cys) a single tRNA is present. In these cases, the wobble anticodon nucleotide (with the exception of tRNA<sup>Cys</sup>) can be modified to more efficiently identify and decode both codons.<sup>8</sup> It is important not to overlook the engineering challenge to ensure that the correct logic is implemented. A particular tRNA anticodon must correctly identify either one and only one mRNA codon, or two, three or four specific ones. Misinterpretation would lead to incorrect protein sequences.

The logic and implementation of synonymous codons is taken up in more detail in part 2. Relying on fewer tRNAs saves the cell energy and material and decreases risk of damaging mutations (the fewer the tRNAs genes, the less which could be damaged). The concept of synonyms also minimizes the damage caused by mutations on protein-coding genes at the synonymous position, since in many cases the correct amino acid would still be identified during translation.

While the advantages just mentioned may be apparent, this requires careful upfront design and will not arise by chance nor evolutionary trial-and-error. Once the genetic code logic was selected, the tRNA ‘hardware’ must be designed able to implement the redundancy logic with high precision. As an example, codon patterns UUU and UUC are meant to both represent amino acid phenylalanine (nucleotides U and C

are to be treated as interchangeable in the third position). But they must not be treated as equivalent in the second and first positions. UCU must be translated as serine and CUU as leucine.

The ‘hardware’ design must ensure that the tRNA anticodon and codon H-bond interactions work exactly as necessary in three dimensions during translation at a specific location in a ribosome. We now see why chemical modifications in tRNAs are vitally important and also foreknowledge of what the ‘natural’ structures would look like for various possible chemical solutions.

Incidentally, not to overlook the obvious, once the tRNA hardware specifications were designed, this must be taken into account. In our example, if amino acid leucine is to be specified, then all incorrect UUU or UUC codons must be modified before ‘going live’. (Acceptable codons for leucine would be UUA, UUG, CUU, CUC, CUA, or CUG). This principle must be applied for all tRNA cases of single, double, triple, and quaternary redundancy for all protein-coding genes throughout the entire genome, to prevent translational chaos.

## II. tRNA maturation processes

tRNAs are composed of 73–90 nucleotides and have a characteristic cloverleaf secondary structure made up of the D-loop, T-loop, variable loop or extra arm, and the anticodon stem-loop (ASL) (see figure 2). Coaxial stacking of the T- and D-loops helps to produce the necessary three-dimensional shape.<sup>7,21</sup>

In bacteria, tRNAs are usually extracted from long transcripts by nucleases. In eukaryotes, however, transcription factors recognize specific sequence patterns shared by all tRNA coding regions to mark the genes as individual transcription units to which transcription factors and Pol III bind.<sup>9</sup> Although little or no critical effort has been invested in challenging the notion of common ancestry for tRNA gene sequences from an evolutionary point of view, one unexpected set of observations has been difficult to overlook. This involves the unrelated ways Gln-tRNA are formed. Genome sequence and biochemical analyses provided a major surprise, revealing that different biosynthetic routes are used in each of the three kingdoms.<sup>22</sup>

These kinds of examples reveal that eukaryotes are based on unique designs and contradict the assumption they evolved from prokaryotes. In fact, the uniqueness of so many eukaryote genes and cellular processing with no plausible relationship to prokaryotes is common knowledge. This has led many to question the notion of common ancestry, as the recent case of Chinese Professor Change Tan who then converted from being a committed atheist and evolutionist to a passionate creation scientist.<sup>23</sup>

Eukaryotic cells employ separate DNA-dependent RNA polymerases (Pol I–III) to transcribe precursors such as



ribosomal RNA (pre-*rRNA*) and mRNA (pre-mRNA). Pol III is dedicated to transcribing small RNAs such as pre-tRNAs.<sup>24,25</sup> The primary product of transcription of a tRNA gene must then be modified to become functional.

The precursors generally contain extra nucleotides at both their 5' and 3' ends and sometimes in the middle, which will be discussed next.

#### Removal of 5' leader sequences from pre-tRNAs

The 5' leader sequence is removed from tRNA precursors by ribonuclease P (RNaseP), an enzyme found in all organisms (figure 3).<sup>21</sup> To date, the only known exception to the requirement for RNase P activity is *Nanoarchaeum equitans*, which presumably can produce leaderless tRNA transcripts.<sup>12</sup> The prokaryotic RNaseP are about 10% protein. Archaeal and eukaryotic enzymes are 50–70% protein, and the proteins are larger and share no sequence similarity to each other or to the prokaryotic proteins.<sup>21</sup> Notice again how the data does not imply common ancestry.

Unexpectedly from an evolutionary point of view, RNase P is a protein-only enzyme (PRORP) in plants. Also remarkably, some RNase P versions in the organelles of various organisms require an RNA component and others don't.<sup>24</sup> Without a collection of functional tRNAs translation cannot occur but the prerequisite processing molecular machines are complex. For example, in budding yeast, the RNase P complex consists of the RNA subunit RPR1, and nine essential proteins.<sup>24,26,27</sup>

Almost all yeast nucleus-encoded tRNAs are transcribed as single pre-tRNAs with ~12 extra leader nucleotides on the 5' end.<sup>25</sup> There are three interesting facts about RNase P in yeast:<sup>25</sup>

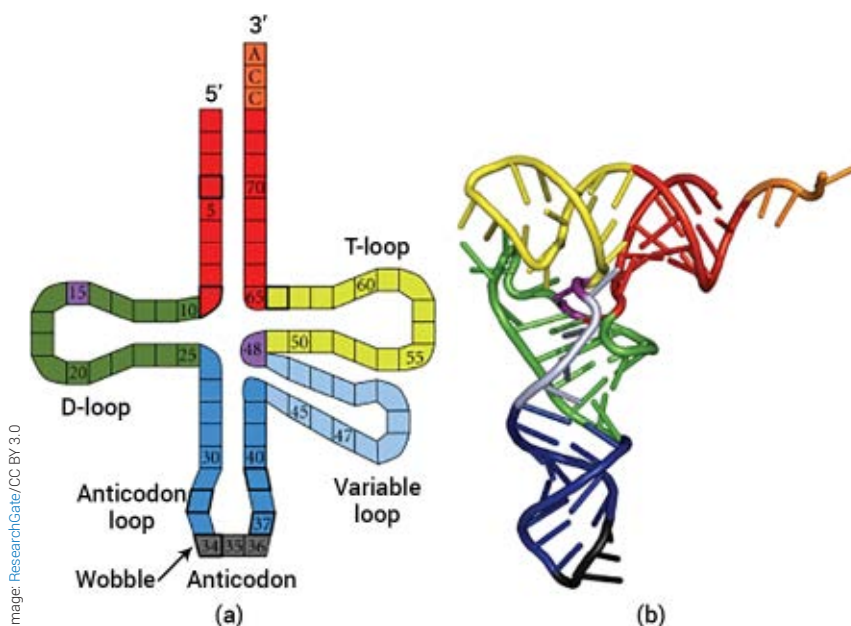
1. Mitochondrial and nucleolar forms of the enzyme are encoded by unrelated genes. Nucleolar RNase P consists of nine proteins and a single essential RNA (RPR1) encoded in the nucleus. In contrast, the mitochondrial enzyme contains only a single nuclear encoded protein, Rpm2, and a single RNA (RPM1). Moreover, RPR1 and RPM1 RNA parts differ extensively in length and sequence.
2. There are extensive differences in RNase P structure when examined using an evolution-theoretic phylogenetic tree. Unlike the bacterial, archaeal, and eukaryotic forms of RNase P, which are ribozymes with varying numbers of protein subunits, higher plant mitochondrial and nuclear versions are now known to be protein enzymes. This is not consistent with a possible evolutionary explanation that mitochondria are the result of endocytosis of aerobic bacteria by large anaerobic bacteria (Boston University biologist Lynn Margulis's Endosymbiotic Theory). A putative single origin of organisms having the genetic code and ubiquitous presence of a ~12 extra leader sequence would predict similar RNase P enzyme complexes throughout nature and not multiple dramatically different designs across various taxa.
3. Most of the protein subunits of the RNase P enzymes are shared with RNase MRP, which is involved in pre-rRNA processing. In other words, the same proteins are involved in producing tRNAs and ribosomes, implying the familiar theme of a concurrent origin of both systems.

For most tRNAs, RNase P generates the mature 5' end. However, generation of the tRNA<sup>His</sup> 5' end requires an additional step, addition of a 5' G ( $G_{-1}$ ), catalyzed by Thg1.  $G_{-1}$  addition to tRNA<sup>His</sup> is essential for its aminoacylation.<sup>25</sup>

#### Removal of 3' trailer sequences

In bacteria and yeast, removal of 3' extensions from pre-tRNA is a biochemically complicated process, involving both exo- and endonucleases.<sup>29,30</sup> In some organisms, exoribonucleases perform 3'-end tRNA processing, while in others, endonucleases do so. Complete 3' processing requires ribonuclease II, polynucleotide phosphorylase, and ribonucleases T and/or PH.<sup>26,27</sup>

Almost all yeast nucleus-encoded tRNAs are transcribed as single



**Figure 2.** tRNAs. (a) Schematic representation, showing the D-loop (green), anticodon loop (blue), anticodon (grey), variable loop (light blue), the T-loop (yellow), the acceptor stem (red), and the CCA aminoacyl binding site (orange). The Levitt base pair is shown in purple. (b) Tertiary structure of a yeast tRNA<sup>Phe</sup>, rendered with PyMOL (1ehz, in the Protein Data Bank).

pre-tRNAs with ~12 extra 3' trailer nucleotides, which need to be removed.<sup>21,25</sup> Yeast Rex1 is a 3' to 5' exonuclease that participates in the processing of pre-tRNA trailers as well as in the processing of other RNAs such as ribosomal 5S rRNA, 5.8S rRNA.<sup>25</sup> Ribosomes without tRNAs serve no purpose, and *vice versa*. We point out that enzymes are precisely designed to operate in both genetic subsystems while avoiding collateral damage to all the other RNA present in the cell. Surely this was so from the very beginning of cells. Or were all these enzymes somehow present before the genetic code and thus when they would be needed?

#### Addition of CCA 3' end

All tRNAs require the CCA sequence at their 3'-end (figure 2). This pattern protrudes from the acceptor stem as a single-stranded motif and is recognized by the aminoacylation enzymes. Once inside the ribosome, the CCA sequence is also necessary to interact with a changing ensemble of ribosomal proteins and RNA elements as the tRNA moves through the ribosome.<sup>31</sup> The CCA end is also necessary for accurate recognition by the RNA component of bacterial RNase P in bacteria.<sup>12</sup>

Remarkably, sometimes this CCA end is encoded in the tRNA genes and other times it must be enzymatically added after the tRNA precursor has been formed, unexpected if a common ancestor had existed. In *E. coli* and related bacteria, the tRNA genes encode the CCA sequence, which is also the case of Gram-positive *Bacillus subtilis* and some related bacteria.

In other Gram-positive bacteria, nearly all eukaryote tRNA genes (both cytoplasm and mitochondria), and archaea, the CCA sequence is not encoded in tRNA genes and must be added post-transcriptionally using a complex series of reactions.<sup>21,25, 31</sup> This sequence is acquired and maintained by stepwise nucleotide addition using an unusual RNA polymerase that does not use a nucleic acid template for nucleotide selection.<sup>31</sup> Kinetic analysis implies additional protein factors assist in the release after CCA has been added.<sup>31</sup>

Further discrediting the notion of common ancestry, bacteria such as *Aquifex aeolicus*, *Deinococcus radiodurans*, and *Synechocystis sp.* use two class II CCA enzymes, one to add C (Cytosine) precisely at positions 74 and 75, and an A (Adenine)-adding enzyme for addition 76.<sup>31</sup> The two enzymes are fundamentally different in the arrangement of secondary structures of individual domains and share virtually no amino acid sequence resemblance.<sup>31</sup>

**Quality control of the CCA sequence.** Even organisms that do encode CCA in tRNA genes contain a CCA enzyme, which is responsible to repair the CCA sequence if damaged.<sup>31</sup> Kinetic work performed on *E. coli* revealed that for each of the three nucleotide additions, the enzyme has an innate ability to discriminate against damaged tRNAs by scrutinizing the integrity of the tRNA substrate. Flawed tRNA can arise from incorrect nucleotide sequences, incorrect processing and folding, and incomplete post-transcriptional

modifications (discussed in part 2). Also, some bacterial and eukaryotic tRNAs carry introns in the anticodon loop that have not been removed.<sup>31</sup> This discrimination causes defective tRNAs to be rapidly degraded by RNA surveillance mechanisms found in all cells, preventing them from entering the ribosome machinery.<sup>31</sup> This will be further elaborated on in part 3 of this series.

Two structurally distinct classes of CCA enzymes are known and they differ in the mechanism of nucleotide selection.<sup>31</sup> The archaeal enzymes are members of class I nucleotidyl transferase family, whereas bacterial and eukaryotic enzymes are members of class II.<sup>31</sup>

Structurally unstable tRNAs are also actively eliminated by CCA-adding enzymes which add a second CCA, leading to a 3'-terminal CCACCA sequence, which serves as a specific degradation tag.<sup>32-34</sup> This occurs in all three kingdoms of life. A study in 2015 using *Archaeoglobus fulgidus* elucidated the mechanism involved.<sup>32</sup> The CCA-adding enzyme monitors in particular the acceptor stem when deciding between CCA and CCACCA addition. The CCACCA addition generates a single-stranded tail that can be recognized by various exonucleases. A recent study showed that tRNAs ending in CCACCA, but not CCA, were degraded *in vitro* by RNase R from *E. coli* and by yeast Rrp44.<sup>33</sup>

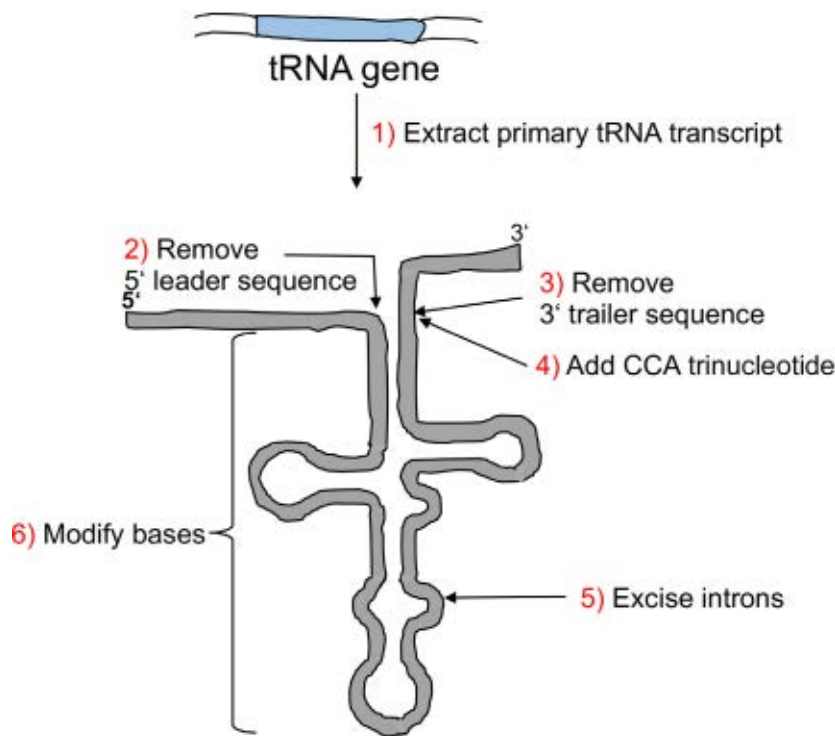
#### Intron removal

tRNA genes often contain introns which must be removed.<sup>21</sup> The percentage of tRNA genes that contain introns varies across organisms, ranging from 0% in some bacteria like *E. coli*, to ~5% in *Drosophila*, *C. elegans*, mouse, and human genomes, to >50% in some archaeal genomes.<sup>24,25</sup> 59 of the 274 yeast nuclear tRNA genes contain an intron, ranging from 14 to 60 nucleotides.

Problematic for evolutionism, there is no similarity in the sequences at the splice junctions.<sup>9</sup> Yeast and vertebrate tRNA introns are always located one base 3' to the anticodon, but introns appear in other locations in tRNA genes in archaea.<sup>25</sup> The catalytic splicing endonuclease subunits are similar across archaea and humans, although the archaeal enzyme recognizes a helix-bulge-helix structure in pre-tRNAs but the budding yeast and human enzymes don't.<sup>9</sup> There also appears to be fundamental differences in the subcellular location of pre-tRNA splicing among different organisms.<sup>9</sup>

Removal of introns from pre-tRNAs in eukaryotes and archaea is performed by a protein-based endonuclease consisting of three polypeptide subunits,<sup>26,27</sup> whereas in bacteria and organelles intron removal proceeds via a group I self-splicing reaction.<sup>9</sup>

Removal of tRNA introns is essential in yeast and other fungi for tRNAs to decode codons. In some cases chemical modifications require the intron to first be removed but several examples are known where essential chemical modifications only occur on intron-containing pre-tRNAs.<sup>25</sup> The implication for these organisms is that both the introns



**Figure 3.** Transcription in eukaryotes produces a pre-tRNA that is cleaved on the 5' end by RNase P and on the 3' end by an endonuclease so that CCA can be attached. Many nucleotide modifications also occur. Many tRNA genes have introns which must be removed.

and the intron-removing enzymes were present from the very beginning.

The pre-tRNA splicing reaction occurs in three steps in yeast, involving several protein enzymes:<sup>25</sup>

1. Remove introns from pre-tRNAs. In yeast and vertebrates, the tRNA splicing endonuclease is composed of proteins Sen2, Sen34, Sen15, and Sen54. Sen15 and Sen54 sequences are very different between yeast and vertebrate cells and are absent from the archaeal genomes.
2. Ligate the 5' and 3' exons. This is a very complex process catalyzed by tRNA ligase Trl1. The yeast mechanism is found also in plants. However, vertebrates and archaea ligate the tRNA halves directly by a 3'–5' ligase activity.
3. Remove the residual phosphate at the splice junction. This is catalyzed by a phosphotransferase.

Thus, even though step one of tRNA splicing is similar for archaea, yeast, plants, and vertebrates, completion of the splicing reaction in yeast and plants requires two steps (5'–3' ligation and 2'phosphotransferase), whereas in archaea and vertebrates, completion requires a single one-step ligation.<sup>25</sup>

#### Preparation of initiator aa-tRNA

Ribosomes must know where to begin translating mRNAs, and the reading frame as units of three nucleotides at a time must begin with the correct single nucleotide. Specially

prepared initiator aminoacyl-tRNAs with a methionine attached are used for this purpose. In archaea and eukaryotes, the initiators are made directly by methionyl-tRNA synthetase, and then bind to initiation factors that deliver them to the ribosome. In bacteria, mitochondria, and chloroplasts the situation is completely different, since the Met-tRNA<sup>Met</sup> produced by the synthetase must first be formylated by a specific formyltransferase before it can be used to initiate protein synthesis.<sup>22</sup> The N-formyl group is removed later from mature proteins by peptide deformylase, leaving the canonical methionine as the mature N terminus.<sup>22</sup>

#### Conclusions

tRNAs are not merely sections of RNA to which activated amino acids are attached. Many protein-based molecular machines are necessary to process the pre-tRNAs and to biochemically transform tRNAs into usable form. The 5' leader sequence must be removed using complex ribonucleases

based on unrelated RNA and protein components across prokaryotes, mitochondria, and eukaryotes. RNase P is a protein-only enzyme (PRORP) in plants, a bad surprise for those believing in the RNA World theory. Removal of 3' extensions from pre-tRNA is a biochemically complicated process, involving both exo- and endonucleases. If evolution is true, what came first, the tRNA genes or the genes needed to process the pre-tRNAs?

The alternative sources of the CCA tag are not predicted by a common ancestor scenario. Suppose the original organisms' tRNA genes included the CCA sequence. What came first, the tRNA genes or the genes necessary to sever the 3'-end of the tRNA precursors at a precise position to expose the CCA tag as a single-strand of RNA? Since the tRNA genes of the archaea, some Gram-positive bacteria, the putative free-living ancestors of mitochondria, and the eukarya lack the CCA motif, were they all mutated away later? This process would have imposed a high cost in energy, material, and reproductive time and thus a selective disadvantage, since during the process of CCA loss the molecular equipment for both CCA-generating options would be needed. Once one scheme of such vital importance for survival worked it should not have changed.

Alternatively, suppose none of the genes contained the CCA initially. What came first, the tRNA genes lacking CCA, the genes to sever the tRNA precursors precisely at



nucleotide position 74, or the gene(s) to add CCA at the severed position?

The fact that bacteria such as *Aquifex aeolicus*, *Deinococcus radiodurans*, and *Synechocystis sp.* don't use one enzyme to repair damaged CCA but have two unrelated enzymes, one to add a 'C' precisely at positions 74 and 75, and the other an 'A' at position 76<sup>30</sup> points to separate designs.

What is the most natural way to explain how adding a second CCA sequence at the 3'-end of tRNAs came about to serve as an information signal, a Boolean yes/no instruction whether to degrade that unstable tRNA? As intelligent agents we frequently use variables to represent objects and events to perform this kind of logic. Evolution would have no plan. All the components to process such logic would need to arise by chance in organisms which supposedly were working just fine before.

In Part 2 we continue by documenting how tRNAs cannot work without dozens of biochemical transformations of the nucleotides, which require protein-based enzymes to have been present from the very beginning.

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# The surprisingly complex tRNA subsystem: part 2—biochemical modifications

Royal Truman

Scores of enzymes are necessary to chemically modify tRNAs since thermodynamic calculations on unmodified sequences rarely predict proper folding into the cloverleaf structure as the ground state. Other modifications are indispensable to permit translation of synonymous codons, translational fidelity of codon–anticodon interaction, maintenance of reading frame at ribosomes, and other cellular processes. Many very complex enzymes are necessary. The yW modification requires 5 polypeptides; t<sup>6</sup>A modification of adenine found at position 37 requires four proteins; and around 25 individual proteins are involved in wobble uridine modifications. The modifications are dynamic, tissue specific, respond to environmental changes, and tRNA concentrations are used as a regulatory signal in several ways to regulate amount of translation.

The cellular genetic system is irreducibly complex, being composed of several collaborating subsystems based on DNA, RNA, and proteins. Genetic code translation cannot occur without tRNAs. In part 1<sup>1</sup> we saw, however, that multiple protein-based molecular machines are also needed to transcribe the tRNA genes, remove 5'-end leaders, 3'-end trailers, remove introns and in many cases add a trinucleotide pattern 'CCA' so that aminoacylation can occur. We also discussed how the CCACCA pattern is added to defective tRNAs which need to be degraded.

Here in part 2 we will see that dozens of biochemical modifications are necessary for tRNAs to function, each of which require a specific protein-based enzyme. As we progress through this series it will become increasingly apparent that the tRNA subsystem must have been planned upfront and many parts introduced simultaneously.

## Post-transcriptional modification. Introduction and overview

Genomes encode scores of enzymes responsible for catalyzing various chemical modifications on tRNAs<sup>2</sup> (figure 1). These modifications can occur on tRNA precursors or fully processed tRNAs.<sup>3</sup> Nucleotide insertions or substitutions are often necessary to ensure base pairing within the tRNA in the three kingdoms of life and that the modifications occur in a stepwise fashion.<sup>4,5</sup>

Some enzymes modify different types of RNA ('dual substrate specificity'). However, most tRNA modification enzymes have unique specificity for tRNA.<sup>7</sup>

Figure 1 illustrates a vitally important insight concerning enzymes, namely their exquisite specificity. Notice that in many cases a methyl group (-CH<sub>3</sub>) is added to different, specific parts of a nucleotide. In cells, thousands of different enzymes are needed with extreme specificity to avoid

damaging the much greater number of possible substrates and positions which should *not* be modified.

Enzymes process individual biomolecules one after the other, carefully rejecting the wrong substrates. This is why they are called molecular machines. The technical challenge to design *de novo* enzymes with no knowledge of what is already found in nature, taking the entire cellular context into account, lies considerably beyond the skills of the best chemists. Contrast typical biological enzymes, which consist of tens of thousands of atoms in the correct positions in three dimensions with the kinds of reagents used by chemists in laboratories. For example, secondary alcohols are oxidized to ketones using reagents like chromium trioxide, CrO<sub>3</sub> (Jones oxidation). This is merely a four-atom reagent which is consumed for each molecule oxidized, with little discrimination among secondary alcohols.

It is now appreciated that tRNA modifications serve many functions including: tRNA discrimination, translational fidelity via codon–anticodon interaction, maintenance of reading frame, tRNA stability,<sup>7</sup> lipid aminoacylation,<sup>8</sup> and bacterial conjugation.<sup>9</sup>

Human nuclear-encoded tRNAs contain on average 13 modifications per molecule, but the number varies considerably.<sup>10</sup> For example, tRNA<sup>Tyr</sup> from placenta has 17 modifications, whereas tRNA<sup>Sec</sup> from HeLa cells has only 3. Mitochondrial tRNAs contain about five modifications per molecule.<sup>10</sup> As of today, <50% of nuclear-encoded human tRNAs have their modifications mapped, and in just one cell type.<sup>10</sup>

Over 140 nucleotide modifications have been identified so far, some of which are conserved throughout all domains of life.<sup>11,12</sup> Nucleotide modifications include base or sugar methylations, base deaminations, base isomerizations, and exotic moiety additions to bases.<sup>7</sup> The anticodon loops of

nearly all tRNAs are heavily modified, predominantly at positions 34 and 37.<sup>11</sup>

Budding yeast has 25 known tRNA modifications, creating tRNAs in which ~15% of the residues are nucleotides other than A, G, U, or C, with an average of ~12 nucleotide modified per tRNA. These modified nucleotides serve important functions including tRNA discrimination, translation fidelity, and tRNA quality control.<sup>7</sup> Many genes are needed to perform these modifications.<sup>7,13</sup>

Approximately 15%–25% of all nucleotides in eukaryotic tRNA contain modifications.<sup>14</sup> These modifications are dynamic, respond to environmental change,<sup>15</sup> and have been proposed to serve various purposes. An important example is discrimination between initiator tRNA<sup>Met</sup> from elongator tRNA<sup>Met</sup> through ribosylation at position A64.<sup>16</sup>

Fully modified tRNAs are invariably more stable than unmodified transcripts.<sup>15</sup> In fact, thermodynamic folding of unmodified sequences only rarely predicts the cloverleaf as a ground state. The chicken-and-egg dilemma is ubiquitous. Most tRNAs will not fold reliably into the correct structure unless properly modified chemically, but the modification protein enzymes depend on correctly functioning tRNAs.

Research continues to reveal ever more differences across kinds of organism. Histidyl tRNAs contain an extra 5'-G nucleotide missing in all other tRNAs. In *E. coli*, the G is derived transcriptionally, and RNaseP does not remove the extra G when it processes the 5' end. In yeast, however, the 5'-most G in the histidyl tRNA is added by a histidyl tRNA guanylyltransferase. The 5'-G of spinach chloroplast histidyl tRNA is derived from the gene, whereas that of animal mitochondria is added post-transcriptionally.<sup>4</sup>

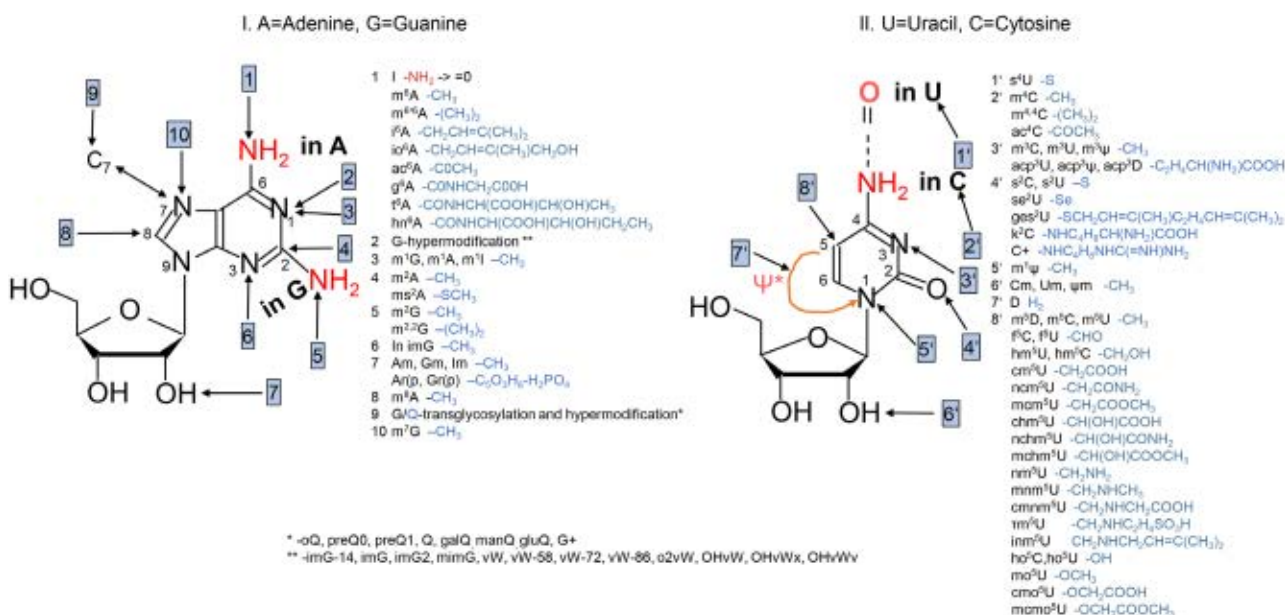
As one would expect from designs which rely on such important modifications, mutations in tRNA and tRNA-processing genes have been linked to many diseases.<sup>16</sup>

*Most modification enzymes are individually unessential.* Despite the important roles played and the fact that many modification enzymes are very similar across broad classes of organisms, most of the yeast genes encoding tRNA modification enzymes are unessential *individually*.<sup>17</sup> In yeast only those responsible for adenosine A34 to inosine I34 deamination (*TAD2* and *TAD3*) and methylation of adenosine m<sup>1</sup>A<sub>58</sub> (*TRM6* and *TRM61*) are known to be absolutely essential.<sup>7</sup> However, severe phenotype deficiencies occur when two or more modification genes of cells are missing or damaged. For example, *PUS1* and *PUS4* are individually unessential genes but the cell is severely defective if both genes are non-functional.<sup>7</sup>

Note that natural selection would not have produced nor fine-tuned an unessential new gene. What is not immediately needed and poses relative selective disadvantages tends to be eliminated from genomes, especially for small, rapidly reproducing organisms. RNA modifications are costly, requiring significant energy for the cell. For example, one biochemical modification, RNA methylation, uses S-adenosylmethionine (SAM) as the methyl donor, and to produce one SAM molecule requires the energy equal to hydrolyzing 12 to 13 ATP molecules.<sup>16</sup>

Complex enzymes are required

Some tRNA nucleotide modifications rely on large, sophisticated modification complexes<sup>13</sup> to cleave, trim, splice,



**Figure 1.** Some of the known biochemical transformations introduced enzymatically during the process of RNA maturation of the four RNA ribonucleosides A, G, C, and U. The scientific names of modified nucleotides are provided in the MODOMICS<sup>6</sup> database. (After Machnicka *et al.*<sup>6</sup>, figure 1)



add terminal nucleotides, and modify specific nucleotide residues through special processing pathways.<sup>18</sup> Most of the modifiers are dynamically regulated in response to environmental cues, often with integrated feedback between many modifications and their pathways.<sup>19</sup>

Many tRNA modification enzymes are composed of a single subunit whereas others require multiple proteins. In the latter case different enzymes often modify chemical groups in a sequential fashion (figure 2). A synthetic natural products organic chemist can best appreciate the brilliance of pathways such as this one, and the absurdity of any claim that the necessary enzymes arose through an unplanned process.

*yW* modification requires 5 polypeptides<sup>7</sup> (figure 2).

Biosynthesis of *mcm*<sup>5</sup>S<sup>2</sup>U<sub>34</sub>, *mcm*<sup>5</sup>U<sub>34</sub> and derivatives requires >25 polypeptides.<sup>7</sup>

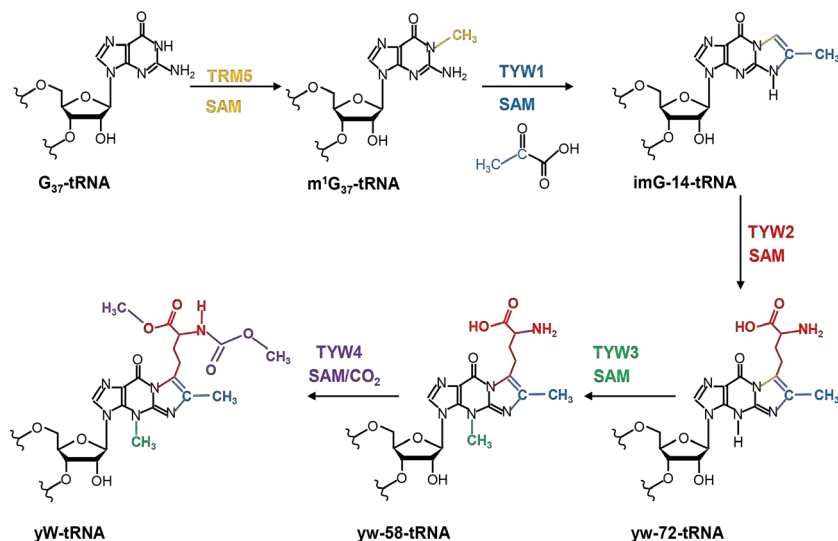
*t*<sup>6</sup>A biosynthesis found at position 37 requires four proteins: YrdC, YgjD, YeaZ, and YjeE in bacteria such as *E. coli*.<sup>11</sup> However, of these four proteins only members of the YrdC and YgjD families are used by all organisms studied so far. The absence of both YeaZ and YjeE in *eukarya* and *archaea* means new genes need to be discovered.<sup>11</sup> This modification prevents formation of a U33-A37 pairing interaction, while allowing cross-strand stacking of A38 and *t*<sup>6</sup>A37 with the first position of the codon. This modification of A (Adenine) is necessary to permit translation of *all* codons with A in the first position.<sup>11</sup> We see once again the chicken-and-egg problem. Without the prerequisite enzyme about a fourth of the codons could not be translated.

*Methylations* at different positions affect multiple properties, including folding details, thermostability, protection from cleavage, and priming for subsequent modifications. tRNA methyltransferases catalyze these reactions.<sup>13</sup>

Pseudouridylation Ψ (C1–C5) is one of the most common alterations. The carbon-nitrogen glycosidic bond (C1–N1) is replaced with a carbon-carbon bond (C1–C5) between the ribose and uracil. This isomerization is catalyzed by pseudouridine synthases (PUS).<sup>13</sup>

*i*<sup>6</sup>A<sub>37</sub> modifications consist of the addition of an isopentenyl group to N6 of adenosine-37 for certain tRNAs, catalyzed by isopentenyl transferases (IPTases).<sup>13</sup>

*Carboxymethylation* (*cm*<sup>5</sup>). In eukaryotes the Elongator complex converts 11 out of 13 yeast tRNAs carrying a U34 in the wobble position. The core Elongator complex (molecular weight of more than 850 kDa) includes two copies of six



**Figure 2.** Sequential biosynthetic pathway of *yW* based on five enzymes (TRM5, TYW1–TYW4). SAM = S-adenosylmethionine. (After Perche-Letuvée *et al.*<sup>35</sup>)

subunits and is regulated by about nine regulatory factors.<sup>13</sup> After the necessary *cm*<sup>5</sup> modification on U34 other enzymatic cascades can then guide additional modifications to produce *mcm*<sup>5</sup>U, *ncm*<sup>5</sup>U, *mcm*<sup>5</sup>S<sup>2</sup>U, *mcm*<sup>5</sup>Um, or *mchm*<sup>5</sup>U. Overall, around 25 individual proteins are involved in wobble uridine modifications, which are very similar among eukaryotes and also have similar counterparts in bacteria and archaea.<sup>13</sup>

Nucleotide modifications necessary for translation to be possible

Each GC base pair in codon-anticodon interactions is held together by three hydrogen bonds (G≡C), whereas AU base pairs use only two (A=T or A=U). This leads to a total of 6 to 9 H-bonds per codon. The difference in free energy due to number of H-bonds or their spatial orientation alone is not enough to ensure sufficient discrimination between correct and wrong codon identification. Cells do not rely on only these H-bond interactions to hold tRNA and mRNA together but rely also on van der Waals forces, steric complementarity, and shape acceptance features.<sup>20</sup>

As an analogy, the need for exact recognition also exists in mRNA regulation by miRNAs (microRNAs). miRNA:mRNA seed regions use 6–8 perfect base-pair matches (unlike only three for codon:anticodon interactions) but even here additional machinery like the RISC complex (RNA-induced silencing complex) is used to ensure reliable interactions. Pairing of 8 perfect matches are indeed more likely to be *bona fide* miRNA targets. Nevertheless, in many cases even perfect 8-nt seed pairing between miRNA:mRNA does not down-regulate the bound mRNA.<sup>21</sup> In a 2019 study, almost twice as many mRNA transcripts having a suitable seed

sequence were shown not to be true targets.<sup>22</sup> Presumably those interactions could be transiently recognized but then dissociate.

Dozens of features within the 21 to 23 nt-long miRNAs contribute to predict true miRNAs, such as: extreme similarity of 8-nt seed for the same gene across many organisms, GC content of target site, UTR length, free energy of seed binding, and distance to UTR end.<sup>22</sup> Clearly there is much more involved in preparing the target for correct recognition than only possessing the seed sequence. The same principle holds also for tRNA anticodon to mRNA codon recognition.

Modification of tRNAs is so important that more genes are devoted to tRNA modification pathways than to the expression of tRNAs themselves. In *E. coli*, for example, 54 of the 61 sense codons are modified taking only nucleotide positions 34 or 37 into account.<sup>22</sup>

#### Modification of anticodon nucleotides to enhance codon–anticodon interactions

The first two nucleotides of mRNA codons are most important in the genetic code. The code redundancy occurs at tRNA position 34, the ‘wobble position’, where often different nucleotides represent the same amino acid. This had led to the so-called revised wobble pairing rules (table 1).<sup>22,23</sup>

Nucleotide 34 undergoes modifications typically required for accurate translation, to permit identification by alternative anticodons. Two examples include modification cmo<sup>5</sup>U34 in tRNA<sup>Ala</sup>(CGU) and mnm<sup>5</sup>s<sup>2</sup>U34 tRNA<sup>Lys</sup>(UUU).<sup>23</sup> (There are special naming conventions for isoacceptors).<sup>24</sup>

Another well-studied example of tRNA modification affecting decoding is the deamination of adenosine (A) to inosine (I) at wobble position 34. Since A only base pairs with U, but I base pairs with U, C, and A, tRNAs with I at the wobble position have an extended codon–anticodon interaction capability (figure 3).<sup>7,25,16</sup>

**Table 1.** Revised wobble pairing rules.<sup>23</sup> Watson-Crick base pairs are shown in italics. Parentheses denote less favoured bindings.

tRNA 5' anticodon base	mRNA 3' codon base (Crick)	mRNA 3' codon base (Revised)
A	<i>U</i>	<i>U, C, G, or (A)</i>
C	<i>G</i>	<i>G</i>
G	<i>C or U</i>	<i>C or U</i>
U	<i>A or G</i>	<i>A, G, U, or (C)</i>
I	<i>A, C, or U</i>	<i>A, C, or U</i>
k <sup>2</sup> C		A
xm <sup>5</sup> s <sup>2</sup> U, xm <sup>5</sup> Um, Um, xm <sup>5</sup> U		A or (G)
xo <sup>5</sup> U		U, A, or G

Given the limited variety of isodecoders, the necessary genes to modify tRNAs at the wobble position were needed from the very beginning. Otherwise translation would have stalled at positions which could not be translated or incorporated the wrong amino acids in the new protein.

#### Modifications in the anticodon arm to enhance codon–anticodon interactions

Nucleotide 37, the residue immediately preceding the first anticodon nucleotide, is modified in >70% of all tRNAs. For example, the m<sup>1</sup>G37 modification is present in ~95% of all known sequences of proline tRNAs.<sup>10,23</sup> Other examples include a 6-threonylcarbamoyladenosine (t<sup>6</sup>A) or a 2-methylthio derivative (ms<sup>2</sup>t<sup>6</sup>A), necessary to recognize AAA or AAG codons. The t<sup>6</sup>A and ms<sup>2</sup>t<sup>6</sup>A modifications help stabilize codon-anticodon pairing.<sup>26,23</sup> Due to the weakness of the A-U hydrogen-bond base, pairings of tRNA<sup>Lys</sup>(UUU) with the AAA codon require modifications at both nucleotides 34 (mnm<sup>5</sup>s<sup>2</sup>) and 37 (t<sup>6</sup>A).<sup>23</sup>

#### Modifications to prevent frameshifting

Other properties can also be affected through modifications outside the anticodon loop, such as stability, ribosome binding, and various translational aspects, for example to prevent frameshifting.<sup>10</sup>

On the other hand, modifications in the anticodon loop can also affect the reading frames during translation. Mutations of the genes responsible for (yW) modification of tRNA<sup>Phe</sup> at position 37 cause increases in -1 frameshifting, useful to compensate for former translation errors.<sup>7</sup>

#### Modification to ensure tRNAs fold correctly

Modifications between the acceptor and D-stem help fold tRNAs into their correct structures and also increase tRNA rigidity.<sup>10</sup> Several modifications hinder canonical base pairing and may facilitate folding into the typical L-shaped tRNA structure by preventing alternative nucleotide pairings or by producing single-stranded regions.<sup>20</sup>

#### Modifications to facilitate tRNA processing on the ribosome

Modifications between the D and anticodon stems increases the stiffness of the modified tRNA, useful to help tRNA on the ribosome adjust to conformational needs on the ribosome during translational elongation.<sup>10</sup>

The well-studied m<sup>1</sup>A58 modification on the T loop, present in almost

all human tRNAs, is essential for the stability of the initiator tRNA<sup>Met</sup>. Adjusting the level of this single modification in specific tRNAs can serve as a rheostat to fine-tune translation rates.<sup>10</sup>

Modifications to permit codon recognition at the P site

Experiments have shown that anticodons including Lys(UUU), Glu(UUC), Gln(UUG), Arg(UCU), and Ala(UGC) in unmodified anticodon stem-loops (ASLs) did not recognize their cognate codons in the ribosomal P site (figure 4) in humans. With the incorporation of s<sup>2</sup>U<sub>34</sub> into the unmodified ASL<sup>Lys</sup>(UUU), the corresponding codons AAA and AAG codons were recognized but not AAC or AAU.<sup>27</sup> Clearly additional factors are needed.

Modifications to permit codon recognition at the A site

ASL<sup>Lys</sup>(UUU) constructs modified with s<sup>2</sup>U<sub>34</sub>, mnm<sup>5</sup>U<sub>34</sub>, or t<sup>6</sup>A<sub>37</sub> combined with codon bound AAA individually and with mnm<sup>5</sup>U<sub>34</sub> and t<sup>6</sup>A<sub>37</sub> when present jointly. In addition, ASL<sup>Lys</sup>(UUU)-s<sup>2</sup>U<sub>34</sub> and ASL<sup>Lys</sup>(UUU)-mnm<sup>5</sup>U<sub>34</sub> t<sup>6</sup>A<sub>37</sub> recognized the AAG codons in the ribosomal A site. Therefore, modifications that restored P site ribosomal codon recognition also restore codon recognition to the ribosomal A site.<sup>28</sup> These examples further suggest upfront design. The 3-dimensional geometry of the A and P sites must be compatible with the sizes and shapes of all tRNAs, taking also chemical modifications into account.

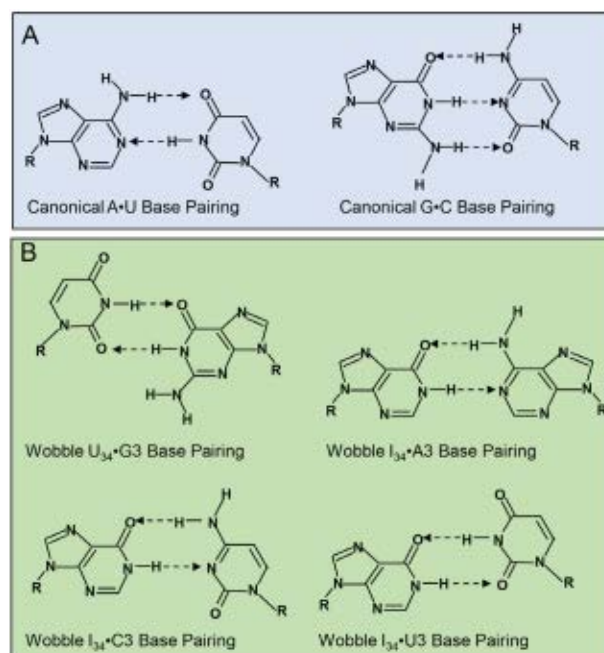
Modifications so each type of tRNA<sup>Met</sup> interacts with correct elongator factor

Modifications serve to discriminate tRNA<sup>Met</sup> species that function in either the initiation or the elongation steps of translation. The initiator and elongator tRNA<sup>Met</sup>, referred to as tRNA<sub>i</sub><sup>Met</sup> and tRNA<sub>e</sub><sup>Met</sup> respectively, have different primary sequences and structures. Using mutagenesis, researchers uncovered that three G-C base pairs in the acceptor stem of the initiator tRNA<sup>Met</sup> are required for proper positioning of the mRNA in the correct reading frame.<sup>28</sup>

Despite these differences, both are aminoacylated by a single methionyl tRNA synthetase, Mes1. They are discriminated during translation via their interactions with translation factors. tRNA<sub>i</sub><sup>Met</sup> interacts with elongator factor 2 (eIF2) and tRNA<sub>e</sub><sup>Met</sup> with elongator factor 1 (eEF1α).<sup>7</sup>

Modifications to compensate for mutations leading to stop codons

A *suppressor mutation*, also called synthetic rescue, is a second mutation that restores the mRNA reading frameshift caused by a preceding shift. This works as long as the portion between the two mutations is not critical for protein function. As an example, frameshift-suppressor variants of tRNA<sup>Pro</sup> contain an extra nucleotide in the anticodon loop



**Figure 3.** Canonical and wobble base pairing of tRNA to mRNA.<sup>26</sup> A: Canonical A•U and G•C base pairs. B: Wobble U<sub>34</sub>•G<sub>3</sub>, I<sub>34</sub>•A<sub>3</sub>, I<sub>34</sub>•C<sub>3</sub> and I<sub>34</sub>•U<sub>3</sub> base pairs. G<sub>34</sub>•U<sub>3</sub> pairings are very rare and not shown. (After Agris *et al.*<sup>27</sup>)

between those in 37 and 38 (referred to as 37.5), and these tRNAs decode CCC-N codons as proline.<sup>23</sup> In the context of tRNA<sup>SufA6</sup>, the inserted G37.5 displaces A38 preventing a U32•A38 pairing. Binding of ASL<sup>SufA6</sup> to a cognate CCG or a +1 slippery CCC-U codon is thereby extremely weak.<sup>23</sup>

Both tRNA<sup>Pro</sup>(CGG) and tRNA<sup>Pro</sup>(GGG) isoacceptors lacking the m<sup>1</sup>G37 modification undergo +1 frameshifting on CCC-N codons. Otherwise, M1 methylation at position 37 stabilizes the interaction with the codon and maintains the mRNA reading frame.<sup>23</sup>

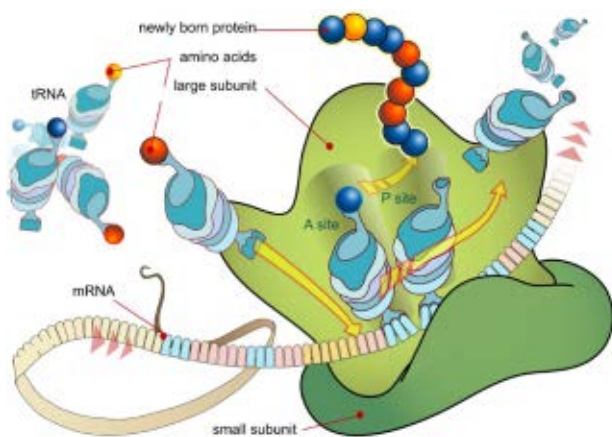
Likewise, the absence of pseudouridine (ψ) at tRNA<sup>Tyr</sup> position 35 or m<sup>5</sup>C<sub>34</sub> in tRNA<sup>Leu</sup><sub>CAA</sub> causes defects in tRNA-mediated nonsense suppression.<sup>29</sup> Defects of Mod5, which catalyzes isopentylation (i<sup>6</sup>A<sub>37</sub>) of a subset of tRNAs also causes a decrease in nonsense suppression of UAA.<sup>7</sup>

Modifications to ensure tRNA stability

Methylation of m<sup>1</sup>A<sub>58</sub> of tRNA<sub>i</sub><sup>Met</sup>, via Trm6/Trm61 catalysis, is essential for that tRNA's stability.<sup>7</sup>

The nucleotide identity of the 32•38 pairing in tRNAs has been found to be predictable on the basis of the strength of the codon-anticodon interaction. For example, the anticodon of *E. coli* tRNA<sup>Ala</sup>(GGC) is stronger due to the three G•C pairs which provide 3 hydrogen-bond interactions per nucleotide between the codon and the anticodon. In this 'strong' case, the 32•38 pairing in tRNA needs to be correspondingly weak. Changing tRNA<sup>Ala</sup>(GGC) from a weak U32•A38 pair to a strong pair such as C32•A38, prevents





**Figure 4.** Translation of mRNA on ribosome. A, P and E sites are shown.<sup>25</sup> A site (for Aminoacyl): The first location the charged t-RNA binds to during translation. P site (for Peptidyl): Holds the tRNA which is linked to the growing polypeptide chain. During the elongation phase, the mRNA advances one codon at a time, coupled with transfer of the tRNA from the ribosomal A to P and P to E sites, catalyzed by elongation factor EF-G. When a stop codon is reached, the peptidyl-tRNA bond is cleaved releasing the new protein. E site (for Exit): The third and last binding site for tRNA in a ribosome during mRNA translation.

the ribosome from being able to distinguish correct from incorrect tRNA-mRNA pairs.<sup>23</sup>

Modifications to produce synonymous codons

In the universal genetic code there are five examples of double redundancy, see table 2: Phe vs Leu; His vs Gln; Asn vs Lys; Asp vs Glu; and Ser vs Arg. Looking more closely, we observe that the first amino acid in each pair is specified by a U or C, and the second of each pair by A or G. Experiments described below show that a single design concept was implemented to ensure this pattern of codon with anticodon recognition.<sup>28</sup>

A key series of experiments in the early 2000s shed light on how a single nucleotide in the wobble position could provide enough binding discrimination. Nucleotide modifications on anticodon position U34 make this possible, specifically chemical modifications  $s^2U34$ ,  $mnm^5U34$ , and  $t^6A37$ .<sup>27</sup>

Modifications to prevent misinterpretation of start and stop codons

Modified methionine is used to identify the start position on mRNAs, and is encoded by AUG. This triplet differs by only one nucleotide at the weak ‘wobble’ position from isoleucine (encoded by AUA, AUU, and AUC). To ensure accurate decoding, in bacteria the isoleucine AUA codon requires a  $k^2C$  modification at position 34. Conversely, *E. coli* elongator tRNA<sup>Met</sup> has an  $ac^4C$  modification at the same position to prevent misreading of the AUA isoleucine codon.<sup>30</sup>

Similarly, modification of position 34 with Cm or Q enable tRNA<sup>Trp</sup> or tRNA<sup>Tyr</sup>, respectively, to discriminate

tryptophan (UGG) or tyrosine codons (UAU and UAC) from stop codons during translation.<sup>31</sup>

Modifications are responsive to environmental changes

Many tRNA modifications are performed dynamically to enhance survival to environmental changes during the organism’s lifetime. For example, several thermophilic bacteria show an increase in tRNA modification levels with growth temperature.<sup>31</sup> In yeast, the tRNA modifications resulting upon exposure to different toxins are considerable and reproducible, revealing an integration with other pathways. In response to oxidative stress induced by hydrogen peroxide, the C34 position of yeast tRNA<sup>Leu</sup>(CAA) is modified by tRNA methyltransferase 4 (Trm4). Furthermore, the amount of  $m^5C$  modification on tRNA<sup>His</sup> rises in response to nutrient depletion and other growth arrest conditions. Another yeast tRNA methyltransferase, Trm9, completes the formation of  $mcm^5U$  and  $mcm^5s^2U$  at the wobble position U34 of tRNA<sup>Arg</sup>(UCU) and tRNA<sup>Glu</sup>(UUC); this methylation prevents cell death by promoting translation of DNA damage response genes that are enriched with arginine and glutamic acid codons.<sup>16</sup>

DNMT2-mediated methylation protects tRNA against stress-induced fragmentation, which is beneficial because tRNA fragments can inhibit the activity of the small RNA processing enzyme Dicer-2 and cause dysfunction of RNA interference.<sup>16</sup> This topic will be followed up on in part 4<sup>31</sup> of this series.

Specialized protein machines known as writers, erasers, and readers of  $m^6A$  are well known for mRNAs. The writer proteins selectively attach ligands, in particular methyl groups. Demethylases balance the methylation stoichiometry of specific mRNAs, often in a pathway- and cell-type-specific manner. The reader proteins execute the biologically intended activities on specific transcripts.<sup>16</sup>

### tRNA concentration used as a regulatory signal

In *E. coli*, accumulation of uncharged tRNAs at the ribosome A site due to amino acid limitation activates a protein called RelA. This RelA synthesizes pppGpp (5’-triphosphate3’-diphosphateguanosine), which initiates a complex process to decrease global gene transcription, while simultaneously stimulating a few genes related to the synthesis of amino acids. Limitation of amino acid availability thus leads to lower levels of rRNA and tRNA synthesis which are not needed by the cell at the time.<sup>3</sup>

In fact, accumulation of uncharged tRNAs serves as an input signal for several pathways that regulate gene expression levels, helping the organism to survive under adverse conditions.<sup>3</sup> In eukaryotes, uncharged tRNAs present due to amino acid deficiency interact with a protein kinase called

**Table 2.** Universal code, showing codon to amino acid mapping. The same amino acid can be coded for by 1, 2, 3, 4, or 6 different codons. The stop signal is represented by 3 codons.

<b>UUU</b>	(Phe/F) Phenylalanine	<b>UCU</b>	(Ser/S) Serine	<b>UAU</b>	(Tyr/Y) Tyrosine	<b>UGU</b>	(Cys/C) Cysteine
<b>UUC</b>		<b>UCC</b>		<b>UAC</b>		<b>UGC</b>	
<b>UUA</b>	(Leu/L) Leucine	<b>UCA</b>		<b>UAA</b>	Stop (Ochre)	<b>UGA</b>	Stop (Opal)
<b>UUG</b>		<b>UCG</b>		<b>UAG</b>	Stop (Amber)	<b>UGG</b>	(Trp/W) Tryptophan
<b>CUU</b>		<b>CCU</b>	(Pro/P) Proline	<b>CAU</b>	(His/H) Histidine	<b>CGU</b>	(Arg/R) Arginine
<b>CUC</b>		<b>CCC</b>		<b>CAC</b>		<b>CGC</b>	
<b>CUA</b>		<b>CCA</b>		<b>CAA</b>	(Gln/Q) Glutamine	<b>CGA</b>	
<b>CUG</b>		<b>CCG</b>		<b>CAG</b>		<b>CGG</b>	
<b>AUU</b>	(Ile/I) Isoleucine	<b>ACU</b>	(Thr/T) Threonine	<b>AAU</b>	(Asn/N) Asparagine	<b>AGU</b>	(Ser/S) Serine
<b>AUC</b>		<b>ACC</b>		<b>AAC</b>		<b>AGC</b>	
<b>AUA</b>		<b>ACA</b>		<b>AAA</b>	(Lys/K) Lysine	<b>AGA</b>	(Arg/R) Arginine
<b>AUG</b>	(Met/M) Methionine	<b>ACG</b>		<b>AAG</b>		<b>AGG</b>	
<b>GUU</b>	(Val/V) Valine	<b>GCU</b>	(Ala/A) Alanine	<b>GAU</b>	(Asp/D) Aspartic acid	<b>GGU</b>	(Gly/G) Glycine
<b>GUC</b>		<b>GCC</b>		<b>GAC</b>		<b>GGC</b>	
<b>GUA</b>		<b>GCA</b>		<b>GAA</b>	(Glu/E) Glutamic acid	<b>GGA</b>	
<b>GUG</b>		<b>GCG</b>		<b>GAG</b>		<b>GGG</b>	

Gcn2p which has a reduced affinity for the charged form of a tRNA.<sup>3,15</sup>

tRNA<sup>Arg</sup> mediates amino-terminal arginylation as a tag for protein degradation. In prokaryotes leucine is used instead of arginine for tRNA-dependent N-terminal modifications.<sup>15</sup>

Various Gram-positive bacteria regulate expression of synthetase genes and genes involved in amino acid biosynthesis by using uncharged tRNAs as an information signal, an example of cellular autoregulation. The Tbox control system involved is integrated with a 200–300 nucleotide regulatory sequence in the 5' untranslated regions of the regulated genes.<sup>3</sup>

## Conclusions

Attachments of specific ligands to tRNAs ensure the proper three-dimensional shape is produced, with the necessary rigidity, ability to interact with several ribosomal components, and with many other cellular processes. In many cases the enzymes involved are very complex. Of vital importance, errors must be prevented in decoding the start and stop codons, which differ by only one nucleotide from coding triplets. The necessary discrimination is provided by modifying key nucleotides using protein-based enzymes<sup>31</sup>

which could not have existed before they were needed by the tRNAs. However, a fundamental principle in biology is that small, rapidly reproducing organisms have a strong drive to streamline their genomes.<sup>32,33</sup> But we see that evolution would require a DNA replicator ‘organism’ preceding the genetic code to possess large amounts of superfluous DNA to be used as the genes to process the tRNAs. Natural selection, however, will favour those replications freed of unnecessary genetic ballast.

The exciting challenge in creation science lies in trying to understand the top down planning and design logic used in cells. This leads to reflection on the tradeoffs involved in alternative solutions, confident that brilliant engineering was involved. The evolutionist can only claim ‘these things just happened’ and allege some evolutionary path must have been followed. This kind of vague thinking offers no research guidance, but the opposite helps develop the kinds of logical thinking so important in developing modern technologies, and cures for diseases. In other words, design analytical skills.

Since evolution lacks planning and foresight the naturalist must invoke what we will call the *Insanely Improbable Chance Change* (IICC) principle. Some biochemical change happened for the first time with an immediate effect of

sufficient benefit for natural selection to act on. For example, at some point for the first time an enzyme catalyzed addition of a second CCA to one or more RNAs, and by miraculous good fortune these just happened to be flawed tRNAs which a cell would be better off without, and astonishingly an unrelated enzyme just happened to recognize the CCACCA pattern and degraded it. These kinds of IICC physical changes must have occurred before any natural selection could begin to act, but the chances of the molecular machines being in place and providing the opportunistic starting point are vanishingly small, all the while avoiding deleterious alternatives. We see this evolutionary assumption every time a code or informative signal is used, for example the N-End Rule to specify half-life of proteins.<sup>34</sup>

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# Is *Morganucodon* a transitional fossil?

Marc Surtees

Evolutionists claim to have good fossil evidence for the transition of synapsids to modern mammals. This includes the key evolutionary transition from creatures with one ear ossicle and a quadrate-articular jaw joint to mammals with three ear ossicles and a dentary-squamosal jaw joint. The evolution of the mammalian jaw joint and middle ear is said to be well-documented and includes *Morganucodon*, which is believed to show a key step in this transition. This review re-examines *Morganucodon* and the claim that it had a transitional double jaw joint and a mandibular middle ear. This claim is essentially guesswork, driven by a prior commitment to evolutionary thinking and is not well supported by the evidence. An alternative view of the evidence is that *Morganucodon* was a mammal and not transitional.

Evolutionists tell us that mammals evolved from the-  
rapsids (which were a type of synapsid) living about 200 million years ago. They claim to have fossil evidence from Mesozoic rocks, showing the evolutionary transition from creatures with one ear ossicle and a quadrate-articular jaw joint to mammals with three ear ossicles and a dentary-squamosal jaw joint. The evolution of the mammalian jaw and middle ear is said to be well-documented and important as a demonstration of transitional forms and exaptation.

Scientists who are not committed to the theory of evolution as an explanation of mammal origins have shown that there is no convincing evolutionary account for the origin of mammals. Bill Mehlert, writing in 1993, reviewed the available evidence and identified many problems which are still relevant today.<sup>1</sup> Eight years later John Woodmorappe published an analysis of the character traits of ‘mammal-like reptiles’ (now referred to as non-mammalian synapsids) and fossil mammals. He showed that instead of gradual evolutionary progression, there are major discontinuities and reversals which seriously undermine the theory that mammals evolved from non-mammals.<sup>2</sup> Evidence from development is also consistent with creation biology.<sup>3</sup>

This article looks again at *Morganucodon* (figure 1), which was claimed to have a double jaw joint.<sup>4</sup> This was purported to be a key step in the evolution of mammals and in particular the evolution of the jaw and middle ear bones, which are some of the defining characteristics of mammals.

## What is a mammal?

A mammal has (among other things) a single jaw bone (the dentary), a dentary-squamosal jaw joint and three ear bones (the malleus, incus, and stapes) which transmit sound from the eardrum, as shown diagrammatically in figure 2. Reptiles, on the other hand, have a jaw made up of several

bones, a jaw joint formed by the articular and quadrate bones and only one ear bone, the columella (sometimes called the stapes), transmitting sound from the eardrum.

Evolutionists believe that mammals evolved from reptile-like therapsid ancestors, which had a jaw similar to reptiles. The ear bones are believed to have been part of the jaw (the mandibular ear) which were connected to a stapes.<sup>5,6</sup> The current evolutionary theory is that the dentary bone increased in size and formed a secondary jaw joint with the squamosal bone. At the same time the two jaw bones involved in hearing (articular and quadrate) are believed to have separated from the jaw and become the malleus and the incus, respectively, of living mammals. Simultaneously, an eardrum evolved as a new sound receiver. However, there are problems with the theory that the mammalian middle ear structures which developed at the angle of the lower jaw were transferred to the basicranium, and there is no clear consensus on the origin and evolution of the mammalian eardrum.<sup>5</sup>

## *Morganucodon*

*Morganucodon* (‘Glamorgan tooth’) is a mammalian genus which supposedly lived during the Late Triassic. According to evolutionists it first appeared about 205 million years ago. It was small, with a skull only 2–3 cm in length and is believed to have looked like a shrew or mouse.

*Morganucodon* is represented by abundant and well preserved, though in the vast majority of cases, disarticulated, material. Most of this came from Glamorgan, in Wales (*Morganucodon watsoni*), but fossils have also been found in the Yunnan province in China (*Morganucodon oehleri*).

The skull of *Morganucodon*

A detailed description of the skull published in 1981<sup>4</sup> is a key publication which is widely quoted. Diagrams from this



Image: Michael B. H. / CC BY-SA 3.0

**Figure 1.** Artistic representation of *Morganucodon watsoni*. Most of its fossil material comes from Glamorgan in Wales, hence the given genus name *Morganucodon* meaning ‘Glamorgan tooth’.

paper are repeatedly redrawn as evidence of a transitional stage in the evolution of the mammalian jaw and ear bones. However, it should be noted that the skull was damaged, and the jaw joint and ear bones were not attached.

#### The jaw joint of *Morganucodon*

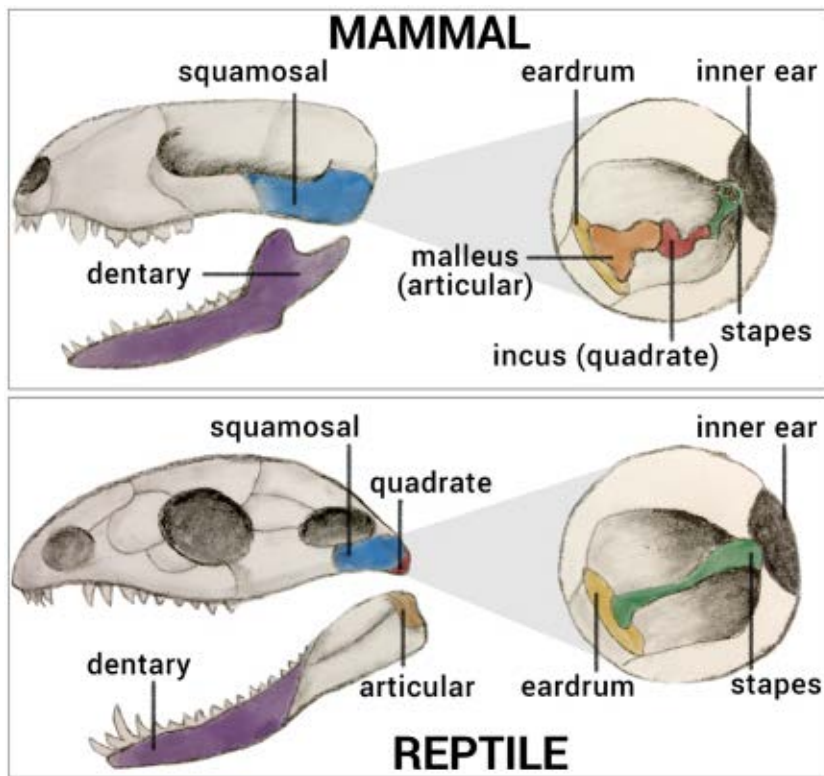
*Morganucodon* is claimed to have had a double jaw joint; that is, both a dentary-squamosal (mammalian) joint and a quadrate-articular (reptilian) joint, which were side by side. However, key parts were missing or disarticulated. The complete lower jaw (dentary) was missing from this specimen and only partial dentary bones have been found. Furthermore, the squamosal, quadrate and articular were not attached, a complete squamosal bone has never been found and all were damaged. Therefore, key parts of the double jaw joint were *inferred*. The supposed double jaw joint is shown in figure 3, which is based on figure 91 from reference 4. Only part of the stapes (yellow) was recovered. The quadratojugal (pink) was never recovered. In addition, the authors write that “the correct orientation of the squamosal was difficult”, which makes their interpretation of the dentary-squamosal joint somewhat subjective.

The quadratojugal bone having never been found presents a very serious problem. Yet the authors stated that “its existence is *certain* from the presence of the facets on the quadrate and the squamosal with which it articulated” [emphasis added]. They go on to write that “The quadratojugal formed the main articulation between the quadrate complex and the squamosal.” It is noteworthy that later publications, which include diagrams redrawn from the publication, simply omit

the quadratojugal, while at the same time maintaining that *Morganucodon* had a double jaw joint. The fact that the reconstruction was based on the belief in the existence of the missing quadratojugal and that it linked the quadrate and squamosal adds to the doubts about the position of the squamosal and seriously undermines the idea of the double jaw joint. If only the quadrate is involved in the proposed joint, this requires a more robust articulation between the quadrate and the articular, which would have limited its movement and consequently reduced the effectiveness as part of the middle ear. However, there is a more serious problem because the quadrate is not large enough to fill the gap between the stapes and the squamosal. Neither can it completely articulate with the articular, which reportedly has two facets, one for the quadrate and another for the quadratojugal. Simply increasing the length of the stapes doesn’t help either, because the dorsal lamina of the quadrate has to fit into the quadrate notch of the squamosal. Not to mention that this would require a rather long stapes, which would be unusual. The question of what the second facet on the articular connects with remains unanswered. All of these problems with the joint between the quadrate and articular are good reasons to conclude that *Morganucodon* had a mammalian jaw joint between the dentary and squamosal alone and calls into question the nature of the quadrate.

#### The middle ear of *Morganucodon*

The questions raised above also have an impact on the claim that *Morganucodon* had a mandibular middle ear involving the quadrate, which functioned simultaneously as



**Figure 2.** A diagrammatic representation of the jaws and ears of mammals and reptiles showing the position and names of different bones

part of the jaw joint and middle ear. Almost all of the middle ear is actually inferred. As mentioned above, the stapes was incomplete as only the footplate has been recovered. Therefore, the length is unknown and the shape of the joint between the stapes and quadrate (q) is unknown. Furthermore, since it is now believed that *Morganucodon* did not have a quadratojugal, the reconstruction is invalid. The initial reconstruction shows a joint between the articular and the quadrate plus the quadratojugal, potentially allowing some freedom of movement for the quadrate as part of an acoustic transformer, but this is now known not to be the case.

Another feature of the reconstructed mandibular middle ear of *Morganucodon* is that the tympanic membrane has been placed in the mandible. But once again this was inferred, because the supporting bones, which are the reflected lamina of the angular and the manubrium, were not recovered. Their shape and location was based on a prior commitment to the theory of the mandibular eardrum as proposed by Allin and others.<sup>5,6</sup>

Furthermore, the evidence for the involvement of the articular is lacking since the complete articular is unknown. The ridge of the articular, which is supposed to have supported the eardrum, is straight, rather than curved, which would make the eardrum a rather odd semicircle. But the

major problem is the lack of fossil evidence for the reflected lamina of the angular and the manubrium; this is enough to cast doubt on the whole idea of a mandibular eardrum. There is also the question of the gap between the quadrate and the squamosal, which suggests that if the quadrate was part of the jaw joint it had to be larger than the bone which had been identified as the quadrate, which in turn calls into question the effectiveness of sound transmission through such a large bone. The whole middle ear assembly is essentially guesswork!

#### The quadrate of *Morganucodon*

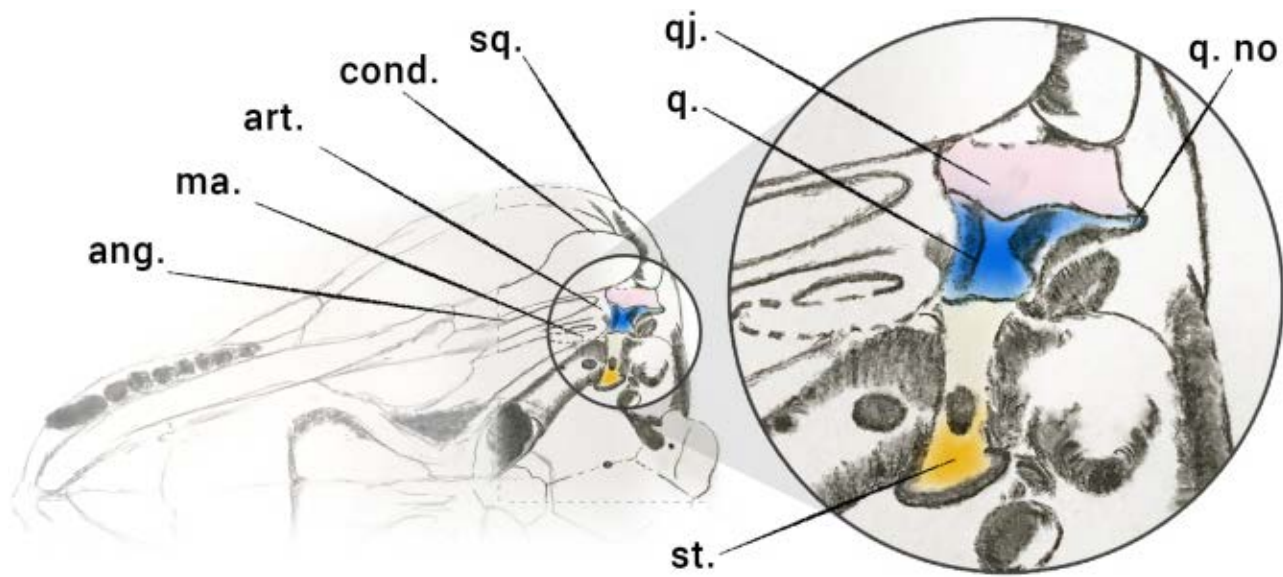
Given the fact that the quadrate is too small and does not have the facets required to articulate properly with the articular, it seems likely that it has been misidentified and incorrectly placed. If the bone in question was actually the incus, then it is possible that the middle ear of *Morganucodon* was essentially a mammalian middle ear. The incus

of mammals is a complex structure which articulates with the stapes and the malleus,<sup>7</sup> and the shape of the quadrate of *Morganucodon* is not dissimilar to the incus of extant mammals, even if it had some rather unusual features. Since the connection with the stapes is unknown and the malleus has never been found it is impossible to know for sure, but the evidence which is available is consistent with *Morganucodon* having had a mammalian middle ear.

In addition, the fact that the petrosal (which houses the inner ear) is described as a ‘fully mammalian petrosal’, also supports this possibility.

Given that the available evidence is more consistent with a mammalian jaw joint, then the suggestion that the element identified as the quadrate is actually the incus is not unreasonable. If this is correct, then the incus was relatively large, but this is consistent with hearing low-frequency sound and would support the idea that *Morganucodon* was a small burrowing mammal. Unfortunately, the malleus and tympanic bone have never been identified, but this is not surprising considering the fragility of these bones. However, it should be noted that there is as much evidence for a mammalian middle ear as there is for the mandibular middle ear. Both theories are valid until further evidence is forthcoming.





**Figure 3.** The reconstructed double jaw joint of *Morganucodon* (based on figure 91 from ref. 4). Left hand side viewed from underneath: ang. = angular; cond. = condyle; art. = articular; ma. = manubrium (infra-articular process); q. = quadrate; q. no. = quadrate notch; qj. = quadratojugal; sq. = squamosal; st. = stapes.

### An alternative interpretation

There are many uncertainties and a lack of clear evidence for the transitional status of *Morganucodon*, so it seems appropriate to suggest an alternative which is consistent with a biblical worldview.

Mehlert examined *Morganucodon* and compared it with the so-called ‘more primitive’ cynodonts (a subgroup of the-rapsids) and concluded that it was most likely a cynodont. Thus, he considered that there was a major gap between *Morganucodon* and mammals. However, he did not consider later research on *Morganucodon* which was published in 1981.

This review looks at the more recent evidence and goes the other way. The weight of the evidence appears consistent with the suggestion that *Morganucodon* was a mammal. Thus, the gap was on the other side, separating *Morganucodon* from the cynodonts. In either case *Morganucodon* was not transitional.

### Conclusion

The argument for *Morganucodon* as a transitional fossil with a double jaw joint, a tympanic membrane (eardrum) in the jaw, and mandibular middle ear bones is clearly a matter of interpretation. Therefore, the case for *Morganucodon* as a transitional fossil is not valid. The evidence is consistent with an alternative interpretation that *Morganucodon* had a mammalian dentary-squamosal jaw joint and mammalian middle ear bones. Therefore, *Morganucodon* was a mammal, and as a result a key step in the evolutionary account of the origin of the mammalian jaw and ears appears to be missing.

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# Ice core oscillations and abrupt climate changes: part 1 – Greenland ice cores

Michael J. Oard

Secular scientists think ice cores are a major challenge to the biblical timescale. However, deep time is automatically built into their analysis of ice cores by using uniformitarian assumptions in the form of flow models and ‘tie points’. They assume the ice sheet has existed for millions of years, and that the annual layers become thinner down the Greenland ice cores. However, annual layer counting is a subjective exercise that is fitted to the assumed age of the core. The GISP2 and GRIP ice cores graphically show numerous abrupt changes in the oxygen isotope ratios, assumed to be correlated to temperature. Many other variables are correlated to the oxygen isotope ratio on the large and small scale. The Younger Dryas event is the last so-called abrupt climate change. Once ‘abrupt climate changes’ were accepted in the Greenland cores in the 1990s, they were then ‘seen’ in many other climate-related records. An isostatic correction was applied to each ice core to determine the elevation of the bedrock at the start of the Ice Age. The low elevation of the deep Greenland ice cores and the warm water surrounding Greenland result in different start times for post-Flood ice buildup.

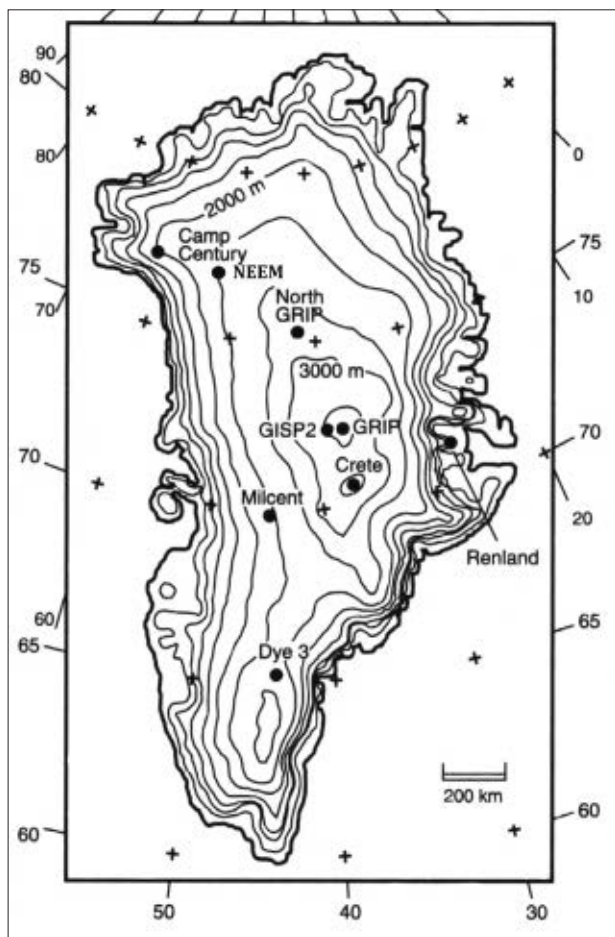
Uniformitarian scientists and popularizers assume that ice cores absolutely disprove the short timescale of the Bible.<sup>1</sup> However, an in-depth analysis of ice cores shows that this is not so.<sup>2</sup> This series will delve deeper into some aspects of ice cores than found in Oard’s 2005 monograph *The Frozen Record*, including one question left for future research: the meaning of the many correlated variables to the isotope ratios on the large-scale and the ‘millennial’ timescale. It will also provide an explanation of the differences between the ice cores on the Greenland and Antarctic Ice Sheets within biblical earth history. Part 1 will describe Greenland ice cores, including two new ones and an explanation for the warmth before glaciation. Part 2 will describe Antarctic ice cores, especially the major difference between the ice cores on the West and East Antarctic Ice Sheets. Part 3 will provide a solution to the large-scale isotopic oscillations and the correlated variables in the ice cores, while part 4 will explain the millennial-scale variations that are different between the Greenland and Antarctic ice cores. Part 5 will explain how the anomalous early Holocene Green Sahara occurred because of the unique conditions of the Ice Age.

## The uniformitarian challenge of Greenland ice cores

Six deep ice cores have been drilled on Greenland (figure 1) since the drilling of the first deep ice core,<sup>3</sup> Camp Century, in 1966. Uniformitarian scientists claim they can actually count 110,000 ‘annual layers’ down to a depth of 2,800 m, near the bottom of the GISP2 ice core drilled near the top of the ice sheet. They believe it is as simple as counting the rings of a tree to determine its age.

However, uniformitarian scientists have assumed that the Greenland Ice Sheet has been more or less in equilibrium (the same size and thickness) for several million years, which means that their ‘annual layers’ would thin considerably down the ice cores (figure 2). Annual layers thin by the weight of the ice above and spread horizontally (figure 3). The final thickness of annual layers depends upon the amount of the ice accumulation and the amount of thinning. The annual layers are distinct near the top of the ice, but with thinning and diffusion deeper in the ice, it can be difficult to interpret them as ‘annual layers’.

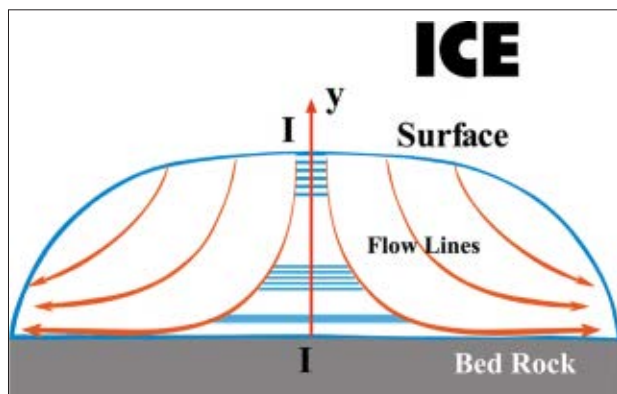
Based on the assumption of deep time and equilibrium for millions of years, uniformitarian scientists have developed flow models. This determines the first guess for their presumed annual layer thicknesses that are believed to thin considerably with depth. These flow models are tuned to other events in uniformitarian earth history, called ‘tie points’, assumed to be accurately dated in other climate records. One tie point is the date of the transition from the last glacial maximum (LGM) to the early Holocene about 15,000 ka. All of these climate records, deep-sea cores, pollen cores, so-called varves, etc., already have deep time and uniformitarianism built in. Is it any wonder that uniformitarian scientists get results that confirm deep time in ice cores? This is why secular scientists and ‘old earth’ creation scientists conclude that ice cores are a fatal flaw to the biblical timescale.<sup>1</sup> The old earth creation scholars need to analyze the ice cores in-depth and stick to biblical earth history, based on the straightforward reading of Scripture. When this is done, an alternative is discovered.



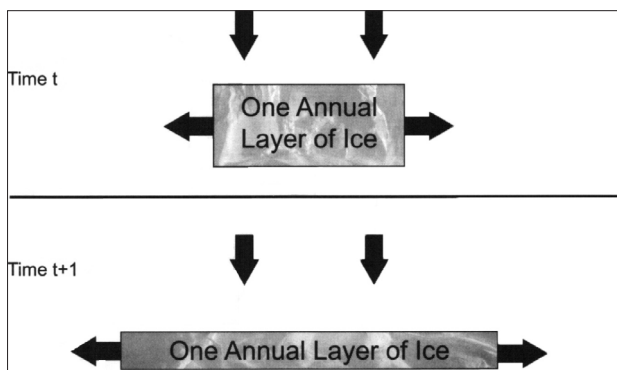
**Figure 1.** Map of Greenland showing ice thickness above sea level with major ice core locations

### Creation-Flood model for the buildup of the Greenland Ice Sheet

The biblical model postulates that the Greenland Ice Sheet grew mostly during the Ice Age, which peaked about 500 years after the Flood in the Northern Hemisphere.<sup>4,5</sup> The ice sheet on Greenland would continue to grow after the Ice Age maximum at the same time as the other Northern Hemisphere ice sheets melted. The continuing above-average warmth of the ocean would have grown the Greenland Ice Sheet, but the growth rate would have decreased with time. Figure 4 presents the postulated increase in the depth of the ice at Camp Century, Greenland, with time after the Flood.<sup>6</sup> From figure 4, the Greenland Ice Sheet at Camp Century did not start building until about 200 years after the Flood and built up rapidly in 300 years to about 1,000 m thick. Camp Century then grew slowly, reaching near-equilibrium at about 3,000 years ago, or 1,500 years after the Flood. The curve shape for Camp Century likely is similar to that of the GRIP, GISP2, NGRIP, DYE-3, and NEEM ice cores, except for likely differences in



**Figure 2.** The uniformitarian long-age ice flow model for an ice sheet in equilibrium for millions of years. Note that the annual layers, showing schematically as horizontal lines down the centre of the ice sheet, thin considerably with depth.



**Figure 3.** One annual layer of ice compressed vertically due to pressure from the ice and snow above. Horizontal lengthening compensates for the vertical shortening.

the timing of the start of ice accumulation. GRIP, GISP2, and NGRIP, being near the centre of the ice sheet, likely started accumulating about 150 years after the Flood. The start of glaciation was delayed because Greenland was surrounded by warm water early in the Ice Age with early glaciation starting in the mountains (which with respect to the bedrock are mostly around Greenland's coasts).

In both the creationist and uniformitarian models, the present-day accumulation is about 0.2 m/yr. Since the very uppermost, most recent layers have experienced almost no thinning, the uppermost annual layer thicknesses (both before and after thinning) should be about the same for both models. However, the deeper annual layers in the biblical model would be much thicker than those presumed from the uniformitarian model. With thinning due to the layers above, the average annual layer from about 175 years, the average beginning of ice buildup at the low elevations, to 500 years would be about 3 m/yr. But if we allow for thinning of the ice, the real annual layer average accumulation would be around 3–6 m/yr for those first 325 years. Part 3 will show that this



is reasonable under the conditions of the Creation-Flood Ice Age. Thinning would be the greatest at the deeper depths in the ice, so the biblical annual layer thicknesses today for about 4,300 years of thinning would be close to that shown in figure 5, which is compared to the secular annual layer thickness due to deep time.<sup>7</sup> How one views the ice sheets, either from the naturalistic or the biblical worldview, determines the results one gets upon analysis.

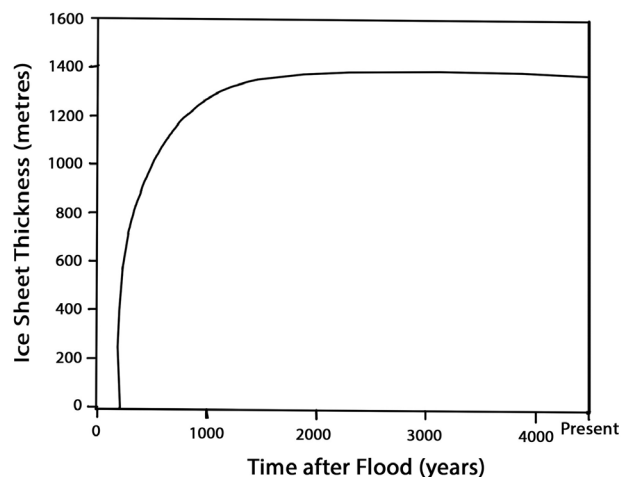
### Uniformitarian ice core years based on assumptions

The uniformitarian scientists have essentially ‘dated’ the Greenland ice cores based on their assumptions.<sup>2,8</sup> This was revealed when they ‘counted’ the annual layers in the GISP2 core (figure 6). The glaciologists arrived at 85,000 years at a depth of 2,800 m. Since this timescale *disagreed* with the timescale based on deep-sea cores and the Milankovitch mechanism, which really ‘dates’ deep-sea and ice cores (see part 2), the researchers went back and ‘re-dated’ the bottom 500 m with a higher resolution laser beam. The laser beam that detects variable dust loading went from 8 mm resolution to 1 mm resolution. Of course, with higher resolution more ‘wiggles’ were detected (figure 7). They ‘discovered’ 25,000 more wiggles, interpreted as annual layers, for an age of 110,000 years at 2,800 m—just the date they needed!<sup>9</sup> This demonstrates one way in which deep time and the Milankovitch assumption influence observations on ice cores.

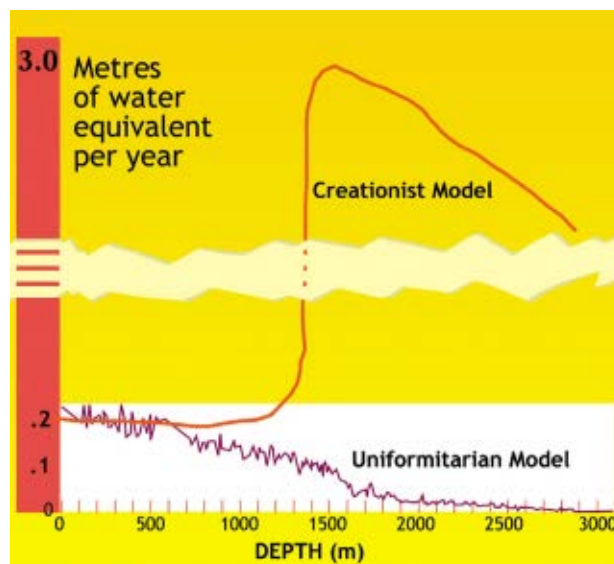
Creation scientists conclude that with an annual accumulation rate of 4–6 m/yr during the Ice Age, wiggles in each annual layer would be multiple storm or within-storm oscillations. The oxygen isotope ratios, one of the variables used in annual layer counting, can vary as much in a storm, due mainly to the warm and cold sectors, as the annual layer.<sup>10,11</sup> Thinning and diffusion would not wipe out such oscillations with such thick annual layers. This especially shows the differences assumptions make in the analysis and results.

### How do so many ice core variables correlate?

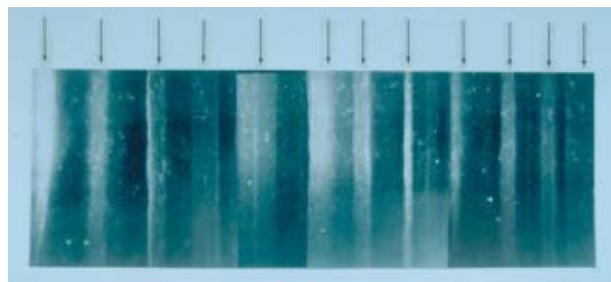
Oard’s 2005 monograph on ice cores, *The Frozen Record*, ended with possibilities for future research.<sup>12</sup> One was finding how carbon dioxide, methane, various chemicals, dust, etc., measured down the ice cores, can be correlated to the oxygen isotope ratios. Many of these variables even correlate with what are believed to be millennial-scale changes. The changes are so rapid that they are called ‘abrupt climate changes’ (figure 8). Uniformitarian scientists have difficulty explaining many of these correlations. How all these variables correlate will be explained within the biblical Ice Age model for the large scale in part 3 and the small scale in part 4.



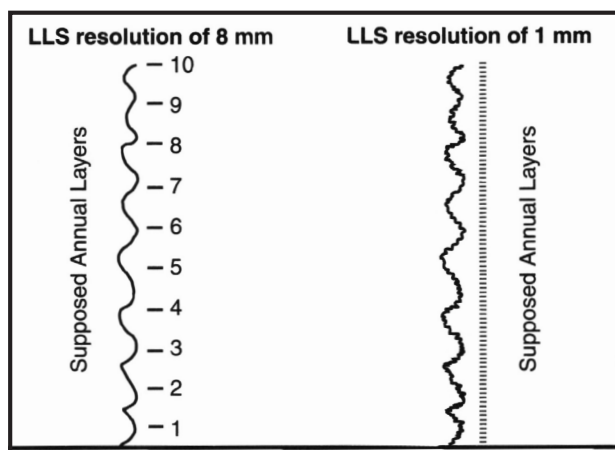
**Figure 4.** The thickness of the Greenland Ice Sheet at Camp Century as a function of time after the Flood (modified from Vardiman,<sup>6</sup> p. 44, and redrawn by Melanie Richard)



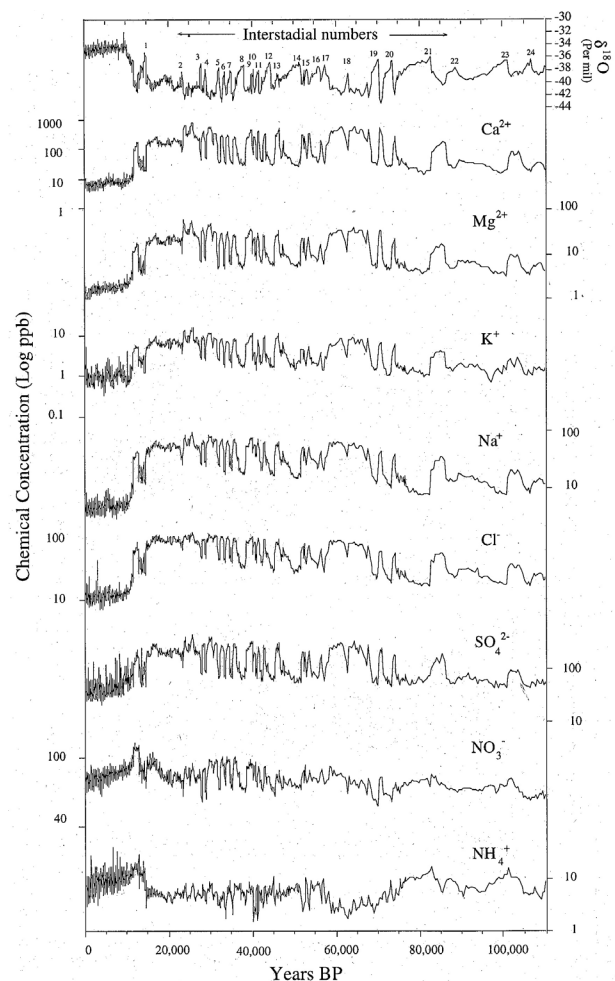
**Figure 5.** The thickness of annual ice layers down the GRIP ice core on central Greenland, calculated according to the evolutionary-uniformitarian model (De Angelis *et al.*,<sup>43</sup> p. 26683) and the biblical Ice Age model



**Figure 6.** Photograph of a 19 cm long section of GISP2 ice core from 1855 m showing annual layer structure illuminated from below by a fibre optic source (NOAA, public domain). Section contains 11 annual supposed layers with summer layers (arrowed) sandwiched between darker winter layers.



**Figure 7.** Schematic of how more 'wiggles' in dust show up when measured at a finer resolution, for example between a laser beam with a width of 8 mm and one of 1 mm. Secular annual layers indicated by short horizontal lines. Although many years are indicated in both curves, such profiles with variable dust wiggles can represent one annual layer or part of an annual layer in the biblical Ice Age model (from Oard,<sup>2</sup> p. 75).



**Figure 8.** The  $\delta^{18}\text{O}$  series from the present to 110,000 years and correlations with various chemical ions in the GISP2 core (from Mayewski *et al.*<sup>17</sup>)

### Abrupt climate changes seen in the Greenland ice cores

In the 1990s, a paradigm shift took place in glacial paleoclimatology.<sup>13</sup> It was discovered from the two deep ice cores, GISP2 and GRIP, drilled 28 km (17 mi) apart at the top of the Greenland Ice Sheet (figure 1), that the oxygen isotope ratio fluctuated abruptly numerous times (figure 9).<sup>14,15</sup> The oxygen isotope ratio is defined as:

$$\delta^{18}\text{O} = \left[ \frac{(^{18}\text{O}/^{16}\text{O})_{\text{sample}} - (^{18}\text{O}/^{16}\text{O})_{\text{standard}}}{(^{18}\text{O}/^{16}\text{O})_{\text{standard}}} \times 1,000\text{‰} \right] \quad (1)$$

It is measured in parts per thousand or per million, and there are several standards.

These oxygen isotope fluctuations are also correlated to changes in other variables such as various chemicals (figure 8).<sup>16,17</sup> The most important ions that determine the origins of many chemicals are sodium and calcium. Approximately 95% of sodium is of marine origin, while almost all calcium is of continental origin.<sup>16,17</sup> High concentrations of these chemicals are correlated with low oxygen isotope ratios for stadials and vice versa for interstadials. Magnesium, potassium, chloride, and sulfate are also correlated with the oxygen isotope ratios and sodium, but nitrate and ammonium are poorly correlated.

Carbon dioxide within the air bubbles in the ice is poorly correlated to the abrupt changes in Greenland cores, but it is supposedly correlated with Heinrich events with amplitude of about 20 ppmv.<sup>18</sup> Carbon dioxide, correlated to the oxygen isotope ratios, also rises about 80 ppmv from the last glacial maximum to the early Holocene, which is considered a mystery.<sup>19</sup> However, the details of carbon dioxide in the Greenland and the Antarctic cores do not match well during the Ice Age. One significant problem, especially in Greenland ice cores, is that carbon dioxide can be altered by dust and in situ chemicals (e.g. sulfuric acid).<sup>20</sup> It is also observed to increase in melt layers. An extreme case of  $\text{CO}_2$  enrichment was shown by a rise of 200 ppm in only 4 cm of core.<sup>20</sup> Organic matter in cores can also affect not only carbon dioxide measurements, but also methane measurements.<sup>21</sup>

Oxygen isotope ratios are also correlated to the amount of dust, with low oxygen isotope ratios, or colder temperatures, generally correlated to high amounts of dust in the Greenland ice cores.<sup>22</sup> Methane, which is generally the same between the two hemispheres, is even more highly correlated to abrupt changes than carbon dioxide (figure 10).<sup>23</sup> It can be used to correlate between the hemispheres.

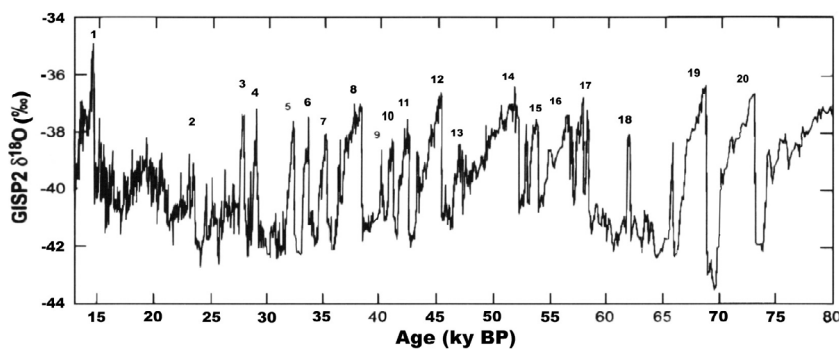
The abrupt changes in the oxygen isotope ratio were noted in the earlier deep Camp Century (figure 11) and Dye-3 (figure 12) ice cores, but little attention was paid to them. To show how uniformitarian and deep time assumptions enter the analysis in the Camp Century ice core (figure 11), figure 13 shows a plot with 'time' and the resulting greatly stretched out lower portion of the ice core.

It was not until the GISP2 and GRIP cores were drilled at the top of the ice sheet that the abrupt oxygen isotope changes really stood out (figures 14 and 9). The abrupt changes are also seen in the new deep ice cores, NEEM and NorthGRIP (NGRIP), drilled north-west of GISP2 and GRIP (figure 1). NEEM and NGRIP ice cores are very similar to GISP2 and GRIP.

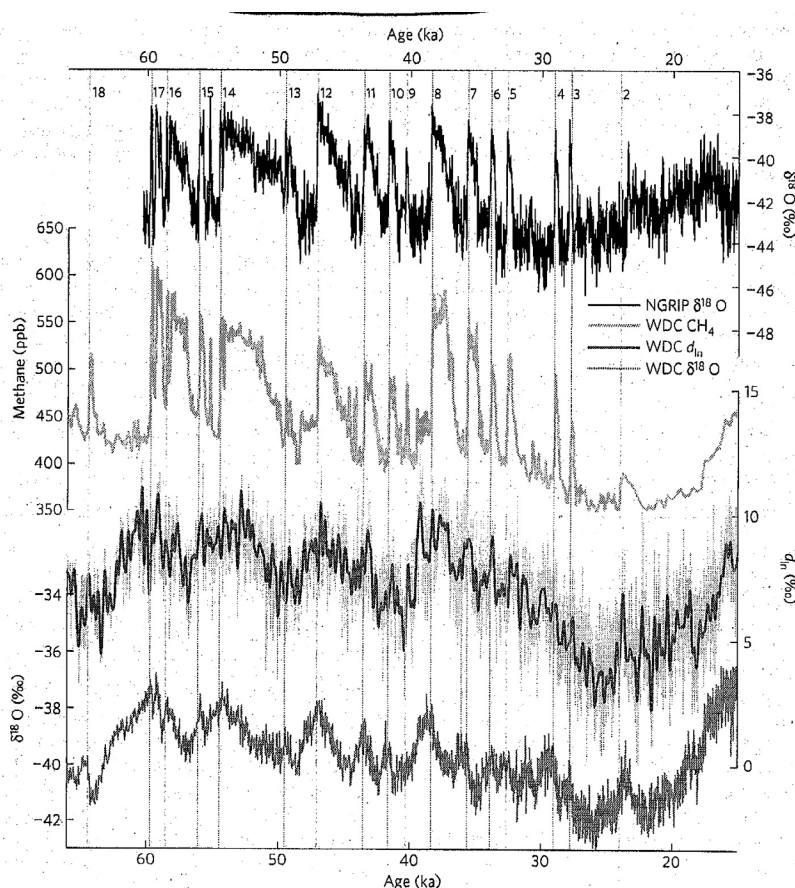
Oxygen isotope ratios are generally correlated to temperature, but there are many other variables that can affect isotope ratios, such as the temperature and oxygen isotope ratio of the evaporating seawater, the distance of travel of the moisture, the latitude, the longitude, the proportion of the precipitation that falls in summer versus winter, the precipitation intensity, the temperature in the cloud at condensation, and the number of condensation cycles.<sup>24</sup> For the sake of discussion, we will assume that the oxygen isotope ratios are proportional to temperature.

If one interprets these oxygen isotope fluctuations just in terms of temperature within the uniformitarian system, it would mean that in the Northern Hemisphere, or at least in the North Atlantic area, the temperatures fluctuated up to 10–20°C on a millennial timescale.<sup>15</sup> However, it was the abrupt rate of change that has startled secular scientists. The rate of change appears to have taken from a decade<sup>25</sup> to as short as 1 to 3 years!<sup>26</sup> The changes lasted for about a millennium or two and then shifted back again to the original oxygen isotope value.

These fluctuations are named Dansgaard-Oeschger (D-O) events after two prominent researchers. It is suggested that the average period of these D-O events is about 1,470 years,<sup>27</sup> and there are about 25 of them (only 20 of them are shown in figure 9).<sup>28</sup> However, some researchers think there is no certain period for D-O events and that they are random.<sup>29</sup> There are also ‘Heinrich events’, based on what are interpreted to be six to eight episodes of ice-rafted debris (IRD) dispersed about every 7,000 to 10,000 years in North Atlantic deep-sea cores.<sup>30</sup> They are believed to have



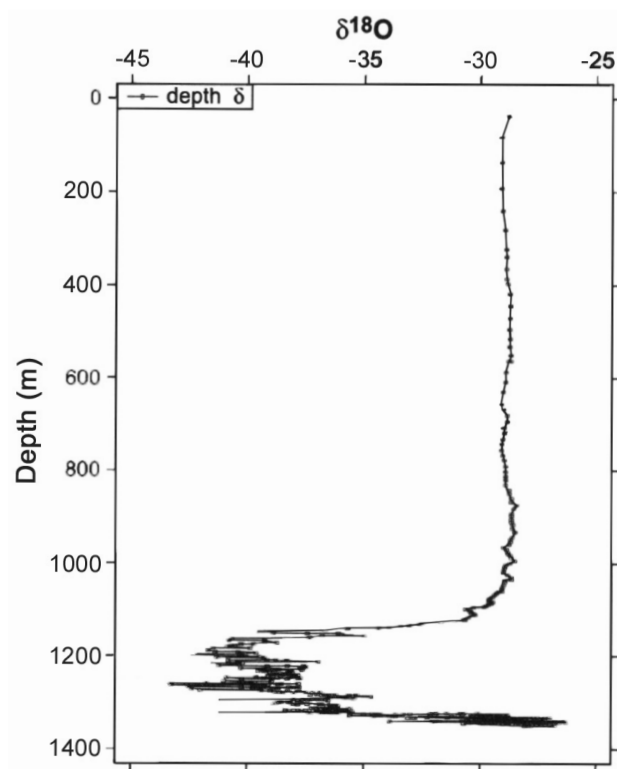
**Figure 9.** Plot of the oxygen isotope ratio fluctuations during the Ice Age portion of the GISP2 ice core, central Greenland according to the uniformitarian timescale in thousands of years (from Schulz<sup>27</sup>). It shows wild abrupt changes. The numbers refer to the Dansgaard-Oeschger events.



**Figure 10.** The NorthGRIP oxygen isotope ratios showing the D-O events that are correlated with methane from the WDC ice core (WAIS Divide) on the West Antarctic Ice Sheet in thousands of years (panels 1 and 2). The third and fourth panels are the deuterium excess and the oxygen isotope ratios on the WAIS Divide ice core (see part 2).

originated from the Hudson Strait Ice Stream. D-O events do not necessarily correlate with Heinrich events.<sup>31</sup> Melting of the Laurentide and Scandinavian Ice Sheets at regular intervals are believed to have discharged an enormous number of icebergs into the North Atlantic Ocean. The icebergs are believed to have rapidly changed the heat exchange over the





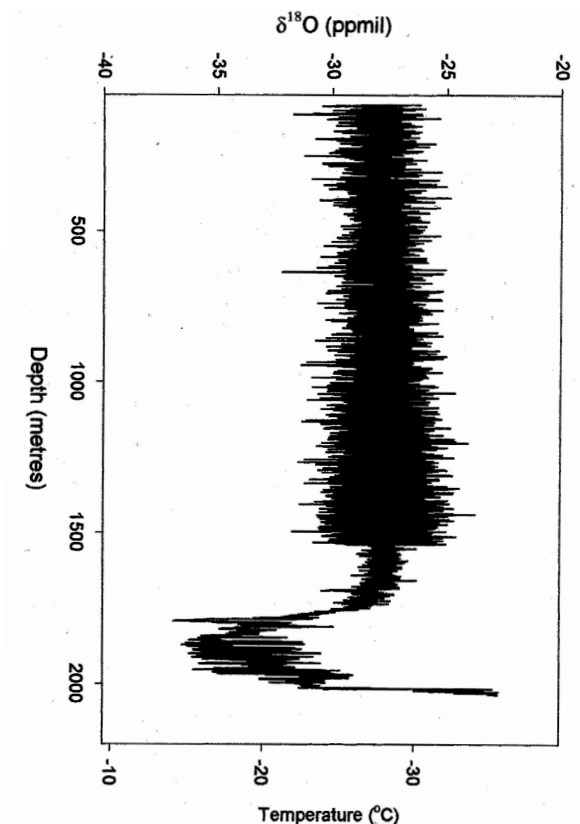
**Figure 11.** The oxygen isotope ratio to bedrock down the Camp Century, north-west Greenland, ice core. Just the average isotope ratio is shown for the layers above 1,100 m (3,600 ft), which is the post Ice Age ice. (From Vardiman,<sup>44</sup> p. 56.)

oceans and cooled the atmospheric temperatures.<sup>32</sup> What is especially perplexing is that one would expect an armada of icebergs during a warm phase, but they surprisingly occur just after extreme cooling and during the millennial-scale cold periods.<sup>33</sup> The data on Heinrich events, of course, depends upon the ‘accurate dating’ of deep-sea cores and identifying true IRDs. The dating of deep-sea cores themselves depends upon evolution, uniformitarianism, and deep time.<sup>34</sup>

### The special Younger Dryas event

One of these abrupt climate changes that had been noticed for a long time, before the 1990s, is the Younger Dryas cold event (figure 15). It is the last cold fluctuation during deglaciation after the warm Bølling-Allerød event. The Younger Dryas is supposed to have lasted about 1,000 to 1,500 years at the very end of the ‘last’ ice age. It had a temperature drop of about 15°C relative to today<sup>35</sup> and is dated about 11,700–12,900 years ago.

Dr Larry Vardiman, formerly of the Institute for Creation Research, believes that changing sea ice areas or an ice shelf change can produce the Younger Dryas cold event.<sup>6</sup> Although it is possible, this hypothesis seems unlikely because the



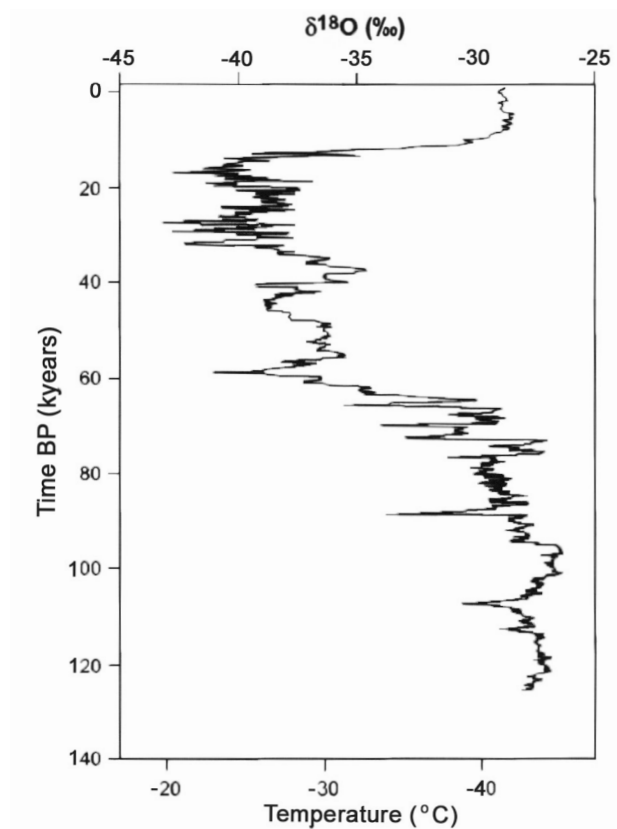
**Figure 12.**  $\delta^{18}\text{O}$  versus depth in the Dye-3 ice core, southern Greenland (from Vardiman,<sup>44</sup> p. 57)

Younger Dryas is similar to all the other abrupt climate changes during the Ice Age, even near the beginning of ice buildup. There would have been no significant sea ice in the early-to-mid Ice Age because of the warm oceans. Sea ice would have increased rapidly during deglaciation since fresh water floats on salt water and freezes more easily. It is likely the sea ice covered a greater area than today by the end of the Ice Age. So, we must look for another mechanism, which will be discussed in part 4.

### Abrupt climate changes suddenly seen in other climatic data sets

It is amazing that abrupt climate shifts were rarely if even seen in other such post-Flood climate records before the GISP2 and GRIP ice cores were drilled. But once those ice cores were analyzed, the idea of catastrophic climate shifts took hold. It is interesting that researchers later ‘discovered’ them in many other climatic data sets on land and sea, for instance in deep sea cores and lake pollen data.<sup>13</sup> They are also seen in the tropics.<sup>36,37</sup> Sarnthein *et al.* state:

“Since these first discoveries from the Greenland Summit cores in the early 1990s, the record of this



**Figure 13.** The oxygen isotope ratio and assumed temperature of snowfall for the Camp Century, north-west Greenland, ice core plotted with uniformitarian time. Notice that the Ice Age portion of figure 8 gets stretched out in time because of their assumptions (from Vardiman,<sup>44</sup> p. 47).

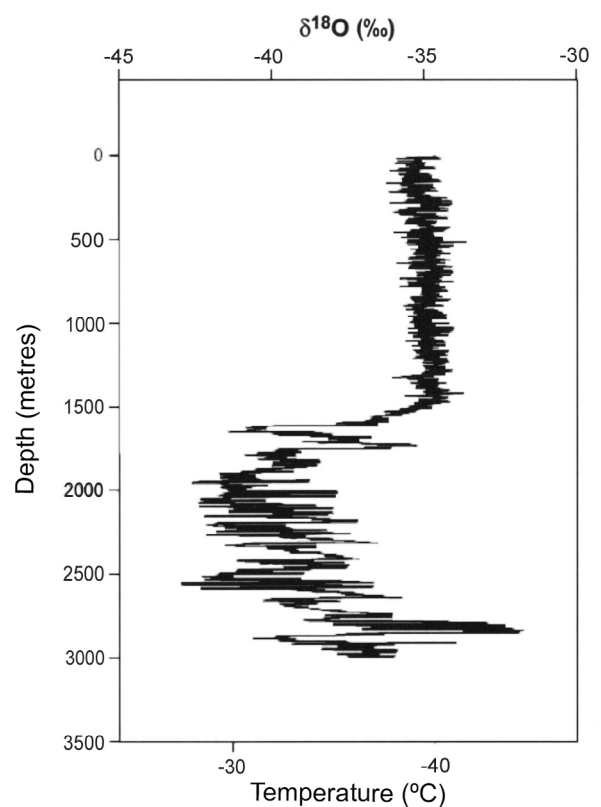
unexpected climatic behavior has been found in many regions, including polar ice sheets; marine sediments of the Atlantic, Pacific, and Indian Oceans; and in terrestrial lakes and bogs.”<sup>38</sup>

Drijfhout *et al.* support this deduction:

“Abrupt climate change is abundant in geological records, but climate models rarely have been able to simulate such events in response to realistic forcing.”<sup>39</sup> Are we witnessing another example of the ubiquitous reinforcement syndrome, where deductions from one data set, abrupt changes, are ‘seen’ in other data sets?<sup>40</sup>

### Isostatic considerations before glaciation

It is important to consider isostatic effects of the ice sheets, since these will be important in explaining the differences between the Greenland and Antarctic ice cores. The time that each Greenland ice core started accumulating ice likely determines the large-scale features of each ice core. We must first correct for isostasy to determine the bedrock elevation *before* the Ice Age. In general, as ice builds up, the bedrock is pushed down by the weight of the ice. The upper



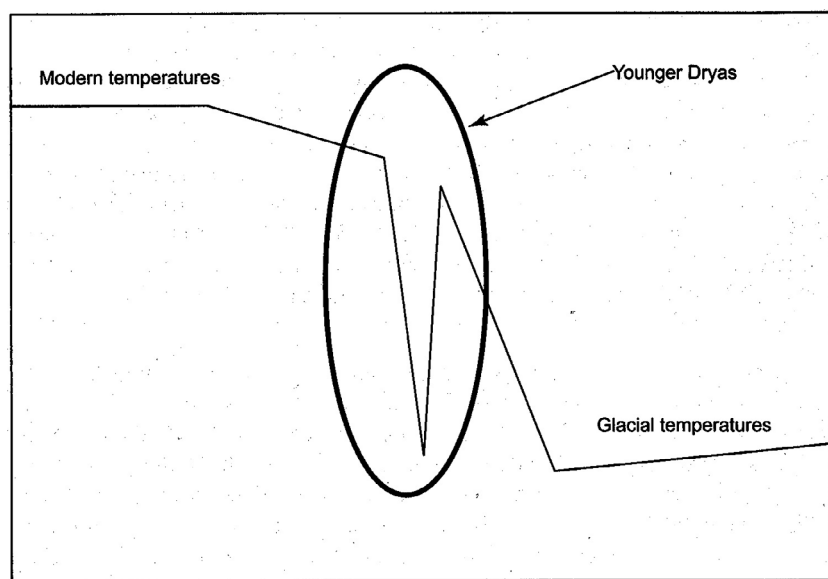
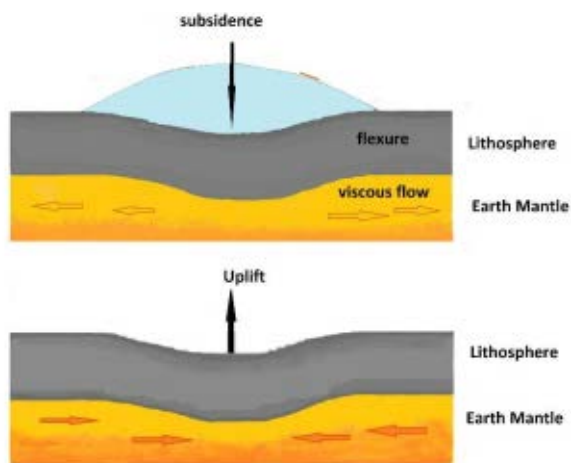
**Figure 14.** The oxygen isotope ratio (top) and the assumed temperature of snowfall from the top of the core to bedrock for the GISP2 ice core at the summit of the Greenland Ice Sheet. Note the widely varying oxygen isotope values in the Ice Age portion of the core below 1,500 m (4,900 ft) (from Vardiman,<sup>44</sup> p. 58).

crust is considered elastic and the up and down motion of the bedrock is called isostasy. The amount of isostatic sinking is believed to be about 1/3 the thickness of the ice above,<sup>41</sup> based largely on the ratio of the density of ice ( $\sim 910 \text{ g m}^{-3}$ ) to that of the asthenosphere ( $\sim 3,300 \text{ g m}^{-3}$ ).<sup>42</sup> So, a 3,000 m thick ice sheet would compress the land about 1,000 m (figure 16). To go backwards to the beginning of ice buildup, we must raise the land by that amount. We will assume that the isostatic change is 1/3 the thickness of the ice at each core location, although isostatic effects are likely caused by more regional ice thicknesses and not point thicknesses. The range of elevation recovery for the Greenland ice core locations ranged from 463–1,110 m.

Table 1 presents the current altitude, ice thickness, present bedrock elevation, isostatic correction, and the height of the bedrock at the beginning of the Ice Age. The lowlands were in general around 1,000 m above sea level (asl) at the beginning. The ice would delay in these lowland locations of Greenland because the snow and ice built up first in the mountains before it spread to the lowlands of Greenland (figures 17–19). The warm water surrounding Greenland held off the ice in the lowlands for a while. Each ice core

**Table 1.** Calculation of the estimated bedrock elevations of Greenland ice core locations before the Ice Age based on an isostatic correction of 1/3 the thickness of the ice

Ice Core	Elevation of ice (m)	Ice thickness (m)	Bedrock elevation (m)	Isostatic correction (m)	Bedrock before Ice Age (m)
Camp Century	1,855	1,390	495	463	958
NEEM	2,450	2,540	−90	847	757
NGRIP	2,921	3,080	−159	1,017	858
GRIP	3,230	3,029	201	1,110	1,211
GISP2	3,208	3,053	155	1,018	1,173
DYE-3	2,486	2,037	449	679	1,128

**Figure 15.** Simplified chart of  $\delta^{18}\text{O}$  and temperature from the end of the Ice Age to today emphasizing the Younger Dryas (YD) cold event after the earlier warm Bølling-Allerød event (from Oard,<sup>2</sup> p. 126)**Figure 16.** Glacial isostasy (drawn by Melanie Richard). In the top diagram, the ice pushes the lithosphere down, but after the ice melts, the lithosphere slowly rebounds upward.

likely started accumulating ice at different times between 100–200 years. It is likely GISP 2 and GRIP glaciated first since they are far from the warm ocean, which is also why the Ice Age ice is thicker there. Camp Century, on the other hand, was close to the warm ocean water and would glaciade later, resulting in a thinner Ice Age portion of the ice core (compare figures 11 and 14).

### Summary

The properties of Greenland ice cores are summarized showing the large-scale and small-scale abrupt change in the oxygen isotope ratios. Deep time is automatically built into Greenland ice cores by assuming the

ice sheet has been in equilibrium for millions of years. This assumption determines the number of annual layers, measured at the top of the ice sheet, that thin with depth. Annual layer counting is shown to be a subjective exercise, assuming deep time, and the astronomical or Milankovitch theory of the ice ages. Many other variables, such as calcium, sodium, carbon-dioxide, methane, and dust, are correlated to the oxygen isotope ratio. The abrupt changes are assumed to be millennial-scale fluctuations in temperature that change abruptly, in years to a few decades. After the discovery of ‘abrupt climate changes’ in GISP2 and GRIP, they were ‘discovered’ in many other climate-related data sets. Isostatic rebound was employed to find the elevation of the ice core locations at the beginning of the Ice Age, which will be important for determining average ice sheet growth and the differences between the Greenland and Antarctic ice cores in part 3.

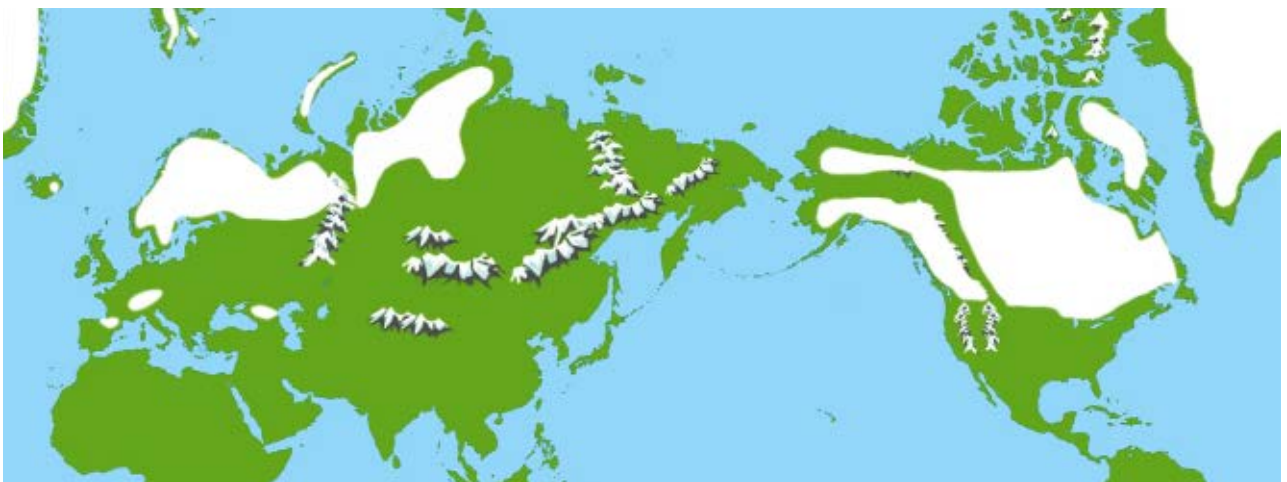




**Figure 17.** Postulated snow and ice after 50 years in the Northern Hemisphere (drawn by Melanie Richard). Notice that only the eastern mountains of Greenland are glaciated.



**Figure 18.** Postulated snow and ice after 100 years in the Northern Hemisphere (drawn by Melanie Richard). Notice that the eastern and south-western mountains of Greenland are glaciated.



**Figure 19.** Postulated snow and ice after 200 years in the Northern Hemisphere (drawn by Melanie Richard). Notice that most of the inland areas and mountains of Greenland are glaciated.

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# Land bridges after the Flood

Michael J. Oard

Biogeography is a difficult subject. Uniformitarian scientists once thought they had the answers with the vicariance hypothesis, but they recently encountered numerous contradictions. Many now support vegetation rafting as a more plausible theory. In the Creation-Flood model, thick log mats left over from the Flood would aid animal dispersal in some cases, but most animals likely made use of land bridges. Two land bridges are discussed in this paper. First, there was a land bridge across the Dover Strait connecting the English Channel, which allowed hippos to migrate into the United Kingdom. Second, the Bering Land Bridge between Russia and Alaska that likely was tectonically raised early in the Ice Age.

**B**iogeography, the study of the geographic distribution of plants and animals around the world, is a difficult subject for both uniformitarian and creation scientists. There are many perplexing observations of present-day and Ice Age distributions of animal and plants. These give rise to many questions, including how marsupials arrived in Australia and South America, and how the now extinct, large mammals arrived in South and Central America.

## Uniformitarian scientists cannot explain biogeography

In the 1960s and 1970s, biogeographers believed that plate tectonics would resolve biogeographic puzzles. They assumed that plants and animals first evolved on a super-continent comprising one land mass, and as this broke up and drifted apart the animals and plants ‘rode the plates’ to their present locations. They thought subsequent evolution of the organisms would explain their present differences on different continents. This is called the *vicariance hypothesis* because plants and animals were passively or *vicariously* transported on the diverging plates.

This theory has suffered in the face of overwhelming opposing evidence<sup>1,2</sup> in DNA comparisons and fossils.<sup>3,4</sup> There are reasons to be suspicious of these fossil comparisons, a subject that is part of *cladistics*.<sup>5</sup> However, some scientists are convinced the method itself is flawed.<sup>6,7</sup> And the molecular data are calibrated with reference to evolutionary interpretation of the geologic and fossil record,<sup>8,9</sup> so an old-age bias is built into the methodology. Regardless of whether these methods are reliable, uniformitarian scientists concluded that many plants and animals did not arrive on the separated continents or oceanic islands until *well after* the break-up of the supercontinent.<sup>10,11</sup> This implies that the plants and animals had to transverse water, and in some cases oceans.<sup>12</sup> Although many anomalies are leading scientists to reject the vicariance hypothesis as the primary explanation for biogeographic distributions, dispersion by rafting is gaining ground.<sup>13</sup> Cowie and Holland summarized:

“We hope, therefore, that the trend identified by de Queiroz (2005)—the resurrection of oceanic dispersal as important in historical biogeography—is real and that the straightjacket of strict vicariance biogeography is being loosened to include once again the plurality of mechanisms and processes that make evolutionary biology the exasperating but ever fascinating discipline that it is.”<sup>14</sup>

Evolutionists are left with three main mechanisms: (1) connections by now submerged land bridges; (2) island hopping across a series of adjacent islands, if close together; and (3) rafting on vegetation, sometimes across vast oceans.<sup>15</sup> Land bridges and island hopping have not become popular ideas, though the Bering Land Bridge is an exception. As a result, many scientists have no choice but to opt for the third option, rafting dispersal, despite it being considered impossible a few decades ago. After all, they abhor a theoretical vacuum.

There have been several recent observations of successful rafting of lizards on pieces of floating vegetation after storms, giving support for rafting. When a hurricane ripped up vegetation on Caribbean islands, some lizards survived on vegetation rafts, and colonized other islands in the area.<sup>16,17</sup> They were rafted only a few hundred kilometres. So, this is a rather trivial example, since it is doubtful these tiny rafts could have crossed an ocean.

Biogeographers have concluded that amphibians like frogs, found on Madagascar and other Indian Ocean Islands, must have been rafted to these islands *several times* despite being unable to tolerate saltwater.<sup>18</sup> Likewise, they think that New World Monkeys (figure 1) were carried from Africa to South America on vegetation rafts.<sup>19</sup> They are likely correct, but the rafts were far larger after the Flood, making the rafting hypothesis much more plausible in a Flood model.

## Creation science challenges

Creation scientists need to explain how air-breathing land animals dispersed from the Ark after the Flood and arrived at far-flung locations. It is controversial whether Paleogene



**Table 1.** Percentage of mammalian megafauna over 44 kg (100 lb) that went extinct during and around the late Pleistocene.<sup>27,28</sup> Southern Eurasia is not included because of insufficient data.

Continent	Percent extinct
Africa	25%
Australia	88%
Northern Eurasia	36%
Northern America	72%
South America	83%



**Figure 1.** A critically endangered Brown Spider Monkey, *Ateles hybridus*, with uncommon blue eyes. Shot in captivity in Barquisimeto, Venezuela.

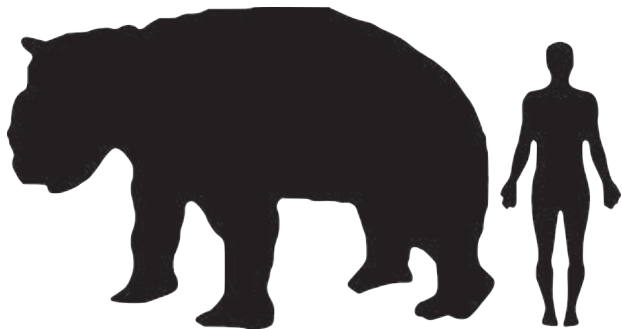
and Neogene animals are post-Flood,<sup>20–22</sup> or from the Flood. I generally favour the latter, though there are exceptions. For the latter option, we need to explain the present and Ice Age distribution of animals and plants. We need to consider the many extinct Ice Age mammals. After the Ice Age, 66% of Ice Age mammals over 44 kg went extinct or disappeared from a continent at the end of the post-Flood Ice Age.<sup>23,24</sup> Many birds and some reptiles also went extinct during this period.<sup>25,26</sup> Table 1 shows the extinctions of mammals on each continent.

The non-glaciated areas during the Ice Age have been described as similar with respect to the variety and number of animals to the Serengeti of Africa.<sup>29</sup> The large mammals living on non-glaciated areas during the Ice Age include the woolly and Columbian mammoths; American mastodons;



Image: Ballistar/CC BY-SA 3.0

**Figure 2.** Skeleton of a large ground sloth from North America (*Megatherium*)



**Figure 3.** *Diprotodon* compared to a human being

various types of huge ground sloths (figure 2); sabre-tooth tigers; cave bears; diprotodons (figure 3); toxodons (figure 4); glyptodons (figure 5); and the so-called Irish elk, which was actually a giant deer (figure 6). We know that toxodons, a large hippo type animal 1.5 m tall with heavy rhinoceros-like body, weighed up to 1,415 kg. They lived in South America during the Ice Age. Arrowheads were found with a few of the toxodon skeletons, indicating post-Flood humans lived alongside of them near the end of the Ice Age.<sup>30</sup> Glyptodons, a strange armadillo-like creature the size of a Volkswagen Beetle weighing up to 2,000 kg, lived mostly in South America. Some South American mammals survive to the present day, including the New World monkeys, tree sloths, and armadillos.

### Dispersal on log mats

Log mats or possibly very large pumice rafts can explain some of the perplexing biogeographic observations.<sup>31</sup> I mentioned back in 1995 that these could aid post-Flood dispersion: “Another application [of the log mat model] is that some of the floating debris likely *survived* the Flood.”<sup>32</sup> Millions of logs of various sizes likely floated on the oceans for a few hundred years after the Flood.<sup>33,34</sup> Even in recent times scientists have reported floating ‘islands’ of vegetation far from land, *often with standing trees and mammalian inhabitants*.<sup>35</sup> Trees can even grow from logs (figure 7). If floating islands exist today after a storm, it stands to reason that a global Flood would create far larger islands. Wood and Murray believe that these log mats would have been thick enough and massive enough to be capable of carrying even large animals.<sup>36</sup>

There is indirect evidence that relatively large mammals were transported across open waters on post-Flood log mats because ground sloths not only colonized South America but also the Caribbean Islands.<sup>37</sup> Sloths in the Caribbean Islands were not nearly as large as the ground sloths in the Americas. The only reasonable way to transport ground sloths and other animals to the West Indies is by rafting.<sup>38</sup>

Transport would begin when a log mat beached, for instance at low tide. Animals would meander onto it. When the log mat resumed floating, possibly after a storm or the rising of the tide, currents would carry the animals to distant shores (figure 8). However, it is questionable that very large Ice Age mammals, like mammoths, could be transported long distances on log mats. The only alternative is dispersal by land bridges.

### Dispersal across land bridges

One of the most effective ways to disperse to the farthest locations from the Ark would have been by land bridges. Three land bridges have been proposed: (1) the connection between continental Europe and England at the Dover Strait; (2) the connection between Asia and North America across the Bering Strait; and (3) the connection or near connection between South-east Asia and Australia. The first two will be discussed in this paper. The third land bridge does not seem plausible because of the many deep, wide ocean channels, but will be discussed further in another paper on the subject of the dispersal of the Australian marsupials.

### The land bridge across the Dover Strait

A land bridge once existed across the Dover Strait connecting the United Kingdom with continental Europe early in the Ice Age.<sup>39</sup> Sonar features of the bottom of the English Channel at and near Dover Strait,<sup>40</sup> the closest approach of England and France, revealed features similar to the



Image: WereSpielChequers/CC BY-SA 3.0

**Figure 4.** Skeleton of a toxodon on display at Bernardino Rivadavia Natural Sciences Museum in Buenos Aires



Image: Ryan Somma/CC BY-SA 3.0

**Figure 5.** A massive glyptodon



Image: Pavel Riha/CC BY-SA 3.0

**Figure 6.** Restoration of the Irish elk





**Figure 7.** A small tree growing from a piling, Willamette River, Oregon (photo courtesy of Ellen Bernert)

Channeled Scablands, the catastrophic deposition and erosion caused by the Lake Missoula flood in eastern Washington.<sup>41,42</sup> Scientists concluded from this and other evidence that a large lake formed in the southern North Sea when the water was blocked by advancing ice in the central North Sea.<sup>43</sup> In the biblical Ice Age model, after the Scandinavian and British-Irish Ice Sheets coalesced the lake would have overtopped the land bridge and destroyed it.

This temporary land bridge surrounded by warm ocean water allowed many animals, including some warmth-loving mammals, to migrate to the United Kingdom early in the Ice Age. Probably the most surprising migrants were hippopotamuses that are found alongside reindeer, musk oxen, and woolly mammoths in England, France, and Germany during the Ice Age.<sup>44,45</sup> Over 100 locations with hippopotamus fossils are found in England alone.<sup>46</sup> Sutcliffe states:

“Finding conditions so favourable the hippopotamus (today an inhabitant of the equatorial regions) had been able to spread northwards throughout most of England

and Wales, up to an altitude of 400 meters [1,300 ft] on the now bleak Yorkshire moors.”<sup>47</sup>

Hippos are intolerant of the cold.<sup>48</sup> The current and historical range of hippos is almost entirely in sub-Saharan Africa. Severing of the land bridge trapped the animals in the United Kingdom. As the Ice Age advanced, animals that require at least a fairly warm environment to survive died together with many large cold-tolerant mammals.

Hippos from interglacials?

Uniformitarian scientists are perplexed by the numerous hippo fossils that lived in England during the Ice Age. They attempt to explain these by arguing that the hippos lived during an interglacial and the cold-tolerant animals in a glacial phase.<sup>49</sup>

“A number of faunal remains have been referred to the Eemian [the ‘previous interglacial’] because of the ‘interglacial’ character of the fauna; solid independent evidence for an Eemian age is, however, sometimes missing.”<sup>50</sup>

Without dates and evidence, they *automatically* pigeon-hole the fauna into interglacial and glacial slots based on their climate preferences. When scientists do this, they miss important clues about the real character of the Ice Age.

Stuart believes that during the ‘last’ interglacial of the late Pleistocene, the Eemian, hippos spread from the Mediterranean region west into France and north up into England.<sup>51</sup> They then disappeared from England supposedly before the last ice age.

Scientists believe we are living in an interglacial, the Holocene. Interestingly, hippos do not live in Europe, the Mediterranean area, or the Middle East today except in protected, artificially warmed zoos. Although the previous interglacial is considered to have been warmer than the Holocene, it is doubtful that hippos would have survived the cool, wet winter climate of England.

Grayson informs us that scientists cannot pigeonhole fossils into interglacials and glacials because the animals are often found *together* in Ice Age sediments:

“In the valley of the Thames [southern England], for instance, woolly mammoths, woolly rhinoceros, musk ox, reindeer (*Rangifer tarandus*), hippopotamus (*Hippopotamus amphibious*), and cave lion (*Felis leo spelaea*) had all been found by 1855 in stratigraphic [sedimentary] contexts that seemed to indicate contemporaneity.”<sup>52</sup>

Mixing to enter glacial sediments?

Some scientists suggest that mixing and reworking of glacial and interglacial sediments can explain why hippo fossils are found in the same sediment as those of cold-tolerant animals. However, this still assumes that the warmth-loving



animals would want to migrate as far north as northern England during an ‘interglacial’. Nilsson states: “The occurrences of such taxa as hippopotamus that are closely adapted to warmth, may result from the reworking of older, interglacial deposits.”<sup>53</sup> However, it is doubtful that evidence for reworking of the sediments really exists.<sup>54</sup> Uniformitarian scientists desire to separate the fauna because of their adherence to long-age uniformitarian assumptions: cold animals prefer glacial climates and warmth-loving animals inhabited warm regions during interglacials. This makes sense in a uniformitarian model that has very cold glacial periods. There is strong evidence against mixing because ‘disharmonious associations’ are *widespread* during the Ice Age and disappear in post-Ice Age sediments.<sup>55</sup>

More evidence against reworking is that mixing itself, supposedly happening during the Ice Age, did not carry over into the present interglacial. Why would ‘mixing’ suddenly stop at the end of the Ice Age?

#### A mild, equable climate during the early Ice Age

The discovery that hippos lived together with cold-loving animals in northern England during the Ice Age indicates the Ice Age climate was quite different from the cold climate the uniformitarian model predicts. Grayson tells us:

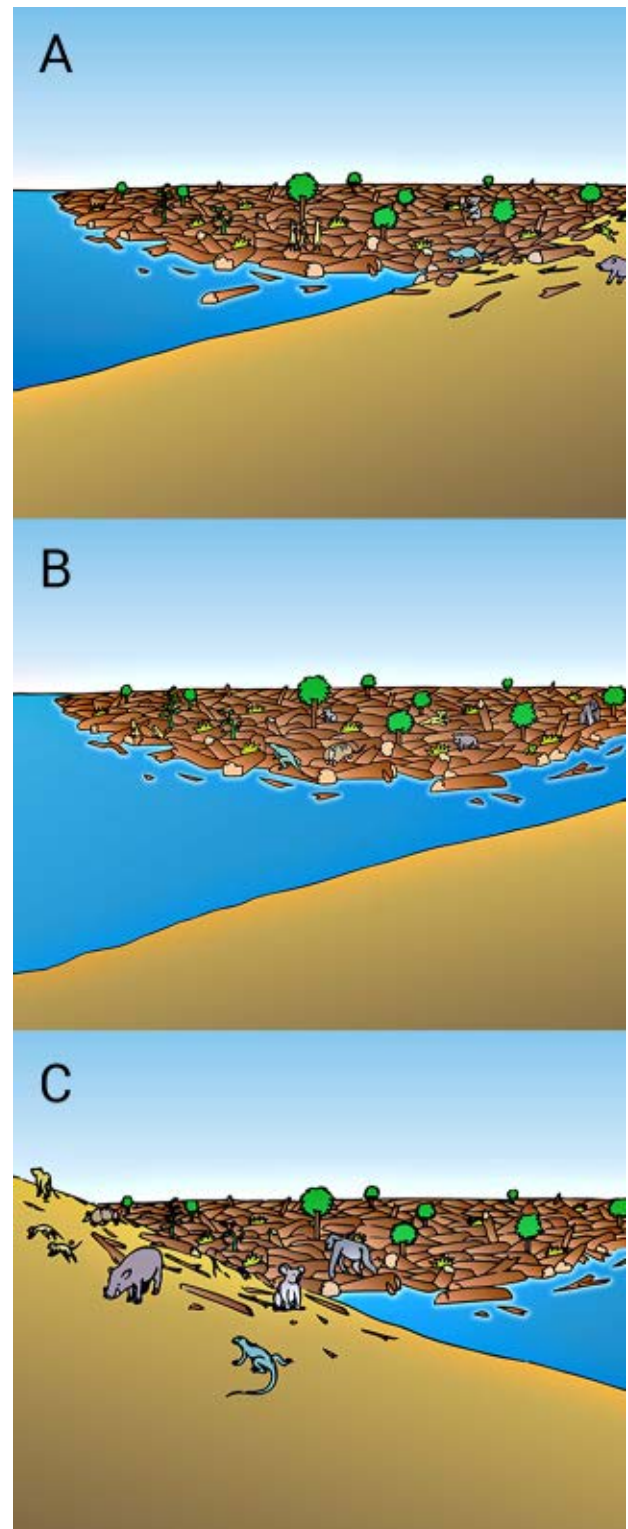
“If the musk ox required cold, and the hippopotamus required warmth, and the stratigraphic evidence implied that they had coexisted, then a straightforward reading of all this information could imply that glacial climates had not, as most felt, been marked by severe winters, but had instead been equable.”<sup>56</sup>

Grayson, quoting from a mid-1800s scientist, further states in regard to the hippopotamus bones associated with cold-tolerant animals in north-west Europe:

“There must have been cooler summers for the reindeer and musk-ox; and on the other hand warmer winters for the hippopotamus and other species whose analogs are today found withdrawn toward the tropical regions.”<sup>56</sup>

As Grayson explains, an equable climate with little seasonal contrast can explain disharmonious associations. It had to have also been a *mild* climate because of the many warmth-loving mammals so far north (figure 9). How could a mild, equable climate occur in England? In uniformitarian thinking it is impossible.

The hippos in north-west Europe, as well as disharmonious associations in general, provide strong evidence against a uniformitarian Ice Age believed to have had much colder summers and winters at mid and high latitudes. Hippos in England as well as other worldwide disharmonious associations are strong evidence that at least part of the Ice Age climate was equable and mild.

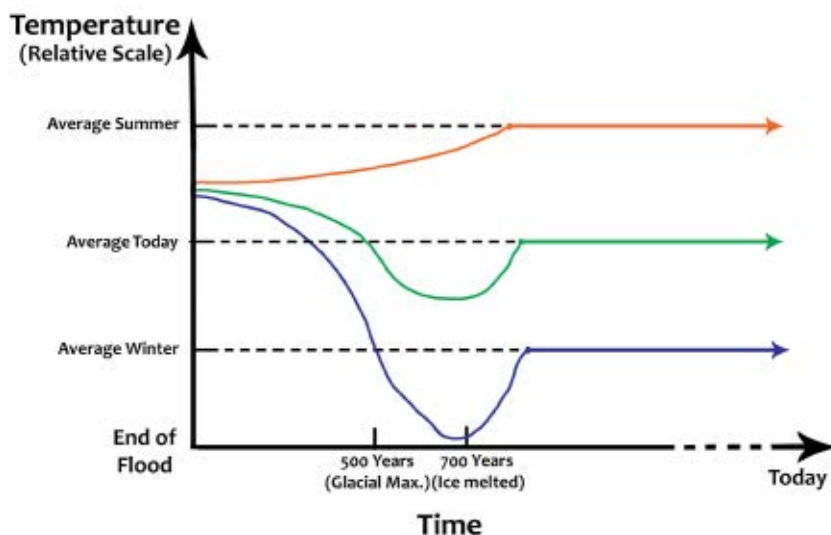


**Figure 8.** Schematic of log mat dispersal of plants and animals (drawn by Keaton Halley).

A) Log mat beached and animals from land walk out onto log mat.

B) The log mat detaches (probably from a rising tide or shifting of the wind) carrying the animals out to sea.

C) Log mat beaches at another location and the animals depart.



**Figure 9.** The postulated average winter, summer, and annual temperature with time for the Northern Hemisphere mid- and high-latitude continents from the end of the Flood through the Ice Age to today (drawn by Melanie Richard)



**Figure 10.** The Bering Land Bridge and the ice-free corridor showing the route of animals and man into the Americas from Eurasia. It is possible man could have taken a coastal route along south-east Alaska, western British Columbia, and into the north-west United States.

The biblical Ice Age model explains the hippos in north-west Europe

The post-Flood climate model can explain why the hippopotamuses and cold-tolerant animals lived together in north-west Europe during the Ice Age. The predominantly westerly winds off of the much warmer Atlantic Ocean early in the Ice Age would create a warm, wet climate in north-west Europe. England's summers and winters may have averaged about 25°C with much more precipitation than today. Hippos could have comfortably spread north-west from the 'mountains of

Ararat' across the Dover Strait Land Bridge into the United Kingdom.

The post-Flood Ice Age climate was very dynamic. After a few hundred years, midway to late in the Ice Age, the ocean cooled so the temperatures over the land also became cooler.<sup>57,58</sup> North-west Europe was increasingly more populated by cold-tolerant animals. Many hippos were able to tolerate some cooling. Glaciation began in the northern mountains of the UK (the Scottish Highlands) about midway into the Ice Age, and then spread into lower elevations and southward. Between this time and late in the Ice Age two things happened. The Dover Land Bridge broke, preventing escape (see above), and the weather had become too cold for the hippos and many of the other mammals. The warm and cold tolerant mammals died together as the climate changed dramatically.

### The Bering Land Bridge?

The Bering Land Bridge aided dispersal of animals to the Americas (figure 10). This land bridge not only exposed the Bering Strait, but also exposed much of the continental shelves of Siberia and Alaska creating a path into the Americas.

Problem of land bridges late in the Ice Age

Before 1930, uniformitarian scientists believed the Bering Sea land bridge was tectonically raised.<sup>59</sup> Now, though, they appeal to multiple ice ages with sea levels dropping as much as

120–130 m to expose the land bridge during the Pleistocene.<sup>60</sup> Before the Pleistocene ice ages, uniformitarian scientists also suggested that the Bering Land Bridge was tectonically raised to aid in the supposed dispersal of Cenozoic animals between Eurasia and North America.<sup>61</sup>

I once believed that the land bridge was exposed late in the Ice Age because of a lower sea level.<sup>57</sup> However, now I think it more likely that it was raised early in the Ice Age for several reasons.<sup>62</sup>

First, the drop in sea level at glacial maximum would have been much less than secular scientists believe. It may

have been only about 50 m, assuming Northern Hemisphere ice sheets were on average about 700 m thick and the Antarctic ice sheet was about 1,200 m thick at glacial maximum (figure 11). There is strong evidence that the Laurentide and Scandinavian Ice Sheets were significantly thinner than secular scientists believe.<sup>63,64</sup> If so, less water would have been trapped in the ice sheets and the oceans would not have been so low at glacial maximum. The current bathymetry of the Bering Strait has a minimum depth of -50 m. If this is true, the Bering Land Bridge would have been barely exposed at Ice Age maximum.

Second, by the time of glacial maximum, the winter temperatures in Siberia, Alaska, and on the Bering Land Bridge would have become too cold (figure 9) for animals to survive the long journey through Siberia to Alaska. Moreover, the atmosphere would have been drier than early in the Ice Age (figure 12) and strong winds with blowing silt and sand would make travel likely impossible.

Third, the ice-free corridor along the east slopes of the Rocky Mountains from the north-west Yukon Territory, south through Alberta, and into Montana (figure 10) would have been closed by the time glacial maximum was reached. This is because by then the two main ice sheets on North America, the Cordilleran Ice Sheet over western Canada (including the Rocky Mountains) and the Laurentide Ice Sheet over central and eastern Canada, would have coalesced.

The Bering Land Bridge tectonically raised early in the Ice Age

Because of the extreme difficulty of crossing the Bering Land Bridge late in the Ice Age, the old uniformitarian idea that the land bridge must have been tectonically raised *early* in the Ice Age seems more plausible. This is especially true since the sea level would have been about 68 m higher than it is today right after the Flood since there were no Antarctic and Greenland Ice Sheets (figure 11).

Several reasons favour this view. First, it is unlikely that God would have told Noah and the animals to spread over the earth knowing there was no way to accomplish this:

“Bring out with you every living thing that is with

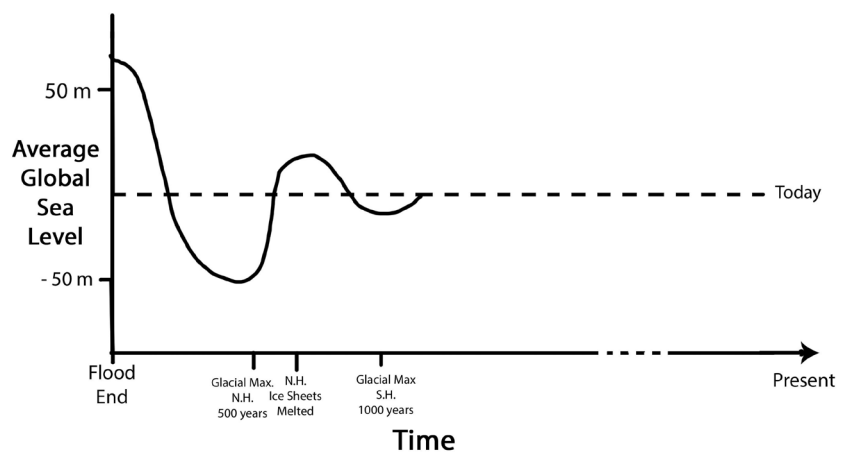


Figure 11. Graph of postulated sea level for biblical history (drawn by Melanie Richard)

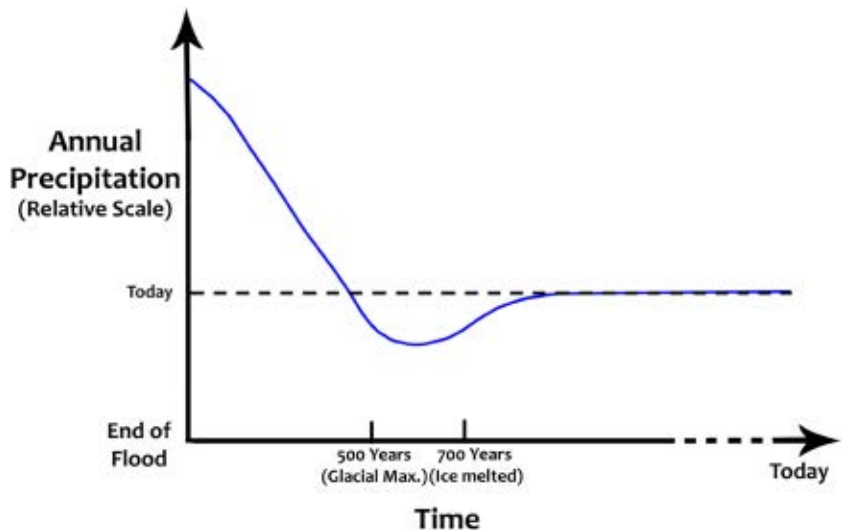


Figure 12. The postulated annual mid- and high-latitude Northern Hemisphere precipitation with time from the end of the Flood through the Ice Age to today (drawn by Melanie Richard)

you of all flesh—birds and animals and every creeping thing that creeps on the earth—that they may swarm on the earth, and be fruitful and multiply on the earth” (Genesis 8:17, ESV).

It is more likely that He would have provided a way to reach Australia and the Americas soon after the Flood.

Second, much warmer winters during the early and middle Ice Age period in Asia and North America (figure 9)<sup>57,58</sup> would allow Ice Age animals, along with animals that cannot tolerate much cold, to cross the Bering Land Bridge into the Americas.

Third, an ice-free corridor from the north-west Yukon Territory to central Montana along the eastern slopes of the Rocky Mountains would have facilitated migration into the central United States and south into South America early in the Ice Age (figure 10).<sup>65</sup> This corridor was likely caused



by downslope, foehn winds blowing from the west, locally called chinook winds. These winds are often strong,<sup>66</sup> warm, and dry, resulting in a thin winter snow cover today that easily melts in the spring. The air would have been fairly warm early in the Ice Age because of the warm North Pacific Ocean.

Fourth, it appears that the post-Flood animals arrived in the Americas early in the Ice Age. One powerful piece of evidence is that Columbian mammoths are found in central British Columbia, the centre of the Cordilleran Ice Sheet, below glacial till. This is evidence of their spread early in the Ice Age.<sup>67</sup> At first this seems contradictory but has an easy explanation. At that time only the mountains of British Columbia were glaciated because the warm onshore flow of air would have kept the lowlands of British Columbia ice free. Some mammoths rounding the Bering Land Bridge and travelling down the ice-free corridor would have passed through the Peace River water gap in the Canadian Rockies and into the lowlands of central British Columbia, before they were covered by ice. Some mammoths died in central British Columbia, before ice filled up the lowlands, leaving their fossils behind under the glacial till.

Did the exotic large mammals in southern North America, Central America, and South America cross the Bering Land Bridge? We do not know for sure, since their fossils are not found along the path. But just because we do not find the fossils of say toxodons, glyptodons, and armadillos in Siberia, Alaska, and in the ice-free corridor, does not mean they did not make the trip. However, some of the large mammals that are found in the Americas have also been found in Siberia and Alaska. Besides indications that the Columbian mammoth made the journey, the ground sloth<sup>68,69</sup> and the American mastodon<sup>70</sup> are found in Alaska and the Yukon Territory as Ice Age fossils. Also found are camels, various horses, the yak, various bison, and the brown bear. The Beringian wolf from the far north made it down as far south as Wyoming.<sup>71</sup> Moreover, fossils of the cave bear found only in Europe and Asia have probably now been found in southern Alberta.<sup>72</sup>

## Summary

Although uniformitarian scientists are perplexed by biogeography, creation science can explain much of it. Giant log mats that were a result of the Genesis Flood would disperse many plants and animals around the world. The Dover Strait Land Bridge early in the Ice Age aided dispersal from continental Europe into the United Kingdom. Even hippos spreading as far as northern England that were eventually entombed together with cold-loving animals later in the Ice Age can be explained. The Bering Land Bridge was likely tectonically raised early in the Ice Age providing a way for animals to rapidly spread from the ‘mountains of Ararat’ into the Americas.

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# New fossil proves turtle evolution ... or does it?

Jerry Bergman

One of the most challenging examples of evolution for its proponents is that of turtles. This is because turtles have a comparatively good fossil record, which shows that even the first claimed turtle is unequivocally a turtle. A review of the newest claims for evidence of turtle evolution, including *Pappochelys*, found that major problems exist with all of the examples reviewed. Rather than confirming evolution the newest fossils do more to reinforce the conclusion that the extant fossil record shows no clear evidence for turtles arising from non-turtle ancestors as postulated by evolutionists.

Turtles are ideal animals for testing the validity of evolution.<sup>1</sup> A major reason is that their hard shells are well-preserved in the fossil record.<sup>2</sup> “Because of their thick bony shells and their compact heavy skulls, turtle remains can survive exposure to the elements much better than” almost any other animal.<sup>3</sup> Once “turtles are present in a fauna, their carapaces, or fragments thereof, stand a reasonably good chance to fossilize.”<sup>4</sup>

Evolutionists date turtle fossils back into the Triassic, evolutionists estimate 220 million years ago, and all turtle fossils, thus far discovered, are clearly turtles.<sup>5</sup> Even the earliest known turtle, the Jurassic turtle called *Kayentachelys*, possessed a “carapace with all of the modern, morphological features of modern, fully aquatic species.”<sup>6</sup> Because the “body plan of turtles is unique among tetrapods”, Darwinists believe turtles are ideal animals for evolutionary studies. Furthermore, “remarkable changes in [both] the skeleton and internal organs” were required to evolve turtles from non-turtles.<sup>7</sup>

## The *Odontochelys* fossil

In 2008, Chun Li and colleagues described a new fossil turtle having unusual features. They named it *Odontochelys semitestacea*, meaning ‘toothed turtle with a half-shell’. The turtle was found in Chinese ocean sedimentary rock that was dated about the same age as one of the oldest known true turtles, *Proganochelys*. *Odontochelys*’ abdomen was protected but it lacked a carapace. The authors’ theory was that turtles evolved their shell piecemeal, the bottom half first.<sup>8</sup> Instead of a carapace, *Odontochelys* possessed only broadened ribs, which one theory speculates eventually coalesced to form larger bony plates (figure 1).<sup>9</sup> The many problems with this theory include:

“How do bones that form in the skin fuse with underlying ribs that normally grow into the lateral body wall? And why is it that uniquely in turtles the shoulder blade lies inside the ribcage, instead of being located outside the ribcage as in all other tetrapods?”<sup>10</sup>

In addition: “Fusion of osteoderms with the underlying ribs would explain how the ribs became incorporated in the carapace”.<sup>10</sup> Another issue was that the 40-centimetre-long creature *Odontochelys* lacked a beak and had a mouthful of well-developed teeth in both its upper and lower jaws in contrast to all known turtles, tortoises and terrapins which instead lack teeth and have powerful horny beaks. This is why “some experts say the fossils raise more questions than they answer ... is *Odontochelys* emblematic of early turtles—or just an oddity? Paleontologists will need to dig up more ancient turtles to find out”.<sup>11</sup> The presence of teeth in *Odontochelys* and lack of a horny beak is evidence that it was a reptile unrelated to turtles.

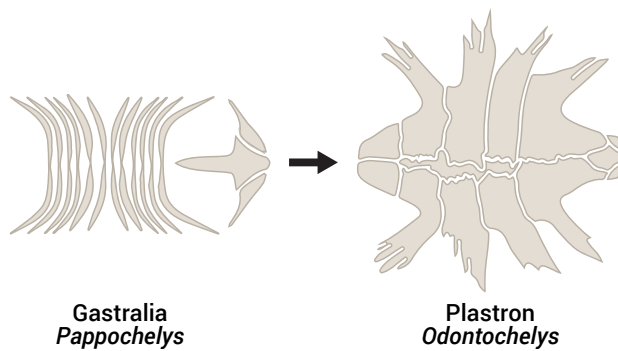
Yet another problem with the evolutionist claim that *Odontochelys* “was clearly a stage between turtles as we know them and their more ancient ancestors”<sup>12</sup> is that it is the only evidence of an animal with broadened ribs. In contrast, all known turtles have a fully developed carapace. No evidence exists for the gradual evolution of broadened ribs or something even close to a carapace and plastron. Ironically, Professor Hans-Dieter Sues, Department of Paleobiology, National Museum of Natural History, in Washington D.C. claims from this sparse and problematic evidence that “The origin and early evolution of the turtle body plan has become one of the best-documented examples of an evolutionary transition in the fossil record”.<sup>12</sup>

## The *Eunotosaurus* claim

Another proposed pre-turtle was *Eunotosaurus* (Latin for stout-backed lizard). It was a typical lizard except that its ribs were wide and flat, forming broad plates.<sup>13</sup> This feature likely was needed to support its very broad and fat body, and was not a precursor of a turtle.

In support of this position, anatomical studies and phylogenetic analyses suggest that *Eunotosaurus* was a parareptile, an animal that existed at the same time as modern turtles, and not a basal turtle, basal meaning the animal that gave rise to modern turtles.<sup>14</sup> When “compared with the





**Figure 1.** Contrast between the gastralia in the *Pappochelys* reptile and the turtle plastron.

newly discovered early turtles”, *Eunotosaurus* was soon judged as “an important part of the turtle’s transformation”.

“All these fossils”, Black claims, “add up to a reasonably clear picture of how the turtle got its shell”, namely “lizard-like reptiles such as *Eunotosaurus* were digging into the ground for food or shelter.”<sup>12</sup> Then, those pre-turtles “with broader ribs would have been more efficient diggers, and this conferred an advantage that was passed down” to its progeny.<sup>12</sup> Exactly how broader ribs made them more efficient diggers is not stated. Effective digging is primarily dependent on muscle development and paw and claw structure, not broader ribs.

Turtle ancestors, evolutionists speculate, must have “evolved an abdomen shell, perhaps to protect and stabilise their internal organs from the stresses of digging.”<sup>12</sup> This improvement would have also been very helpful for other digging animals. Riley Black speculates that the carapace evolved when “bits of bone began to form along the skin of their backs, creating a more enclosed carapace” and “motions required for digging are similar to those that turtles use to swim”.<sup>12</sup> This “pre-adapted turtles to be competent swimmers when that evolutionary niche became available.”<sup>12</sup> Black admits that turtle shell evolution is still very debatable:

“... there is still debate about whether the top half of the shell evolved before or after turtles began swimming. Increasingly shelled-in turtles would have had protection from attack while suspended in the water, but it is unclear whether that was a reason they took to a life aquatic or rather a downstream effect of that move.

Part of the reason we don’t have firm answers here is that there are tens of millions of years between *Eunotosaurus*, *Odontochelys*, and *Proganochelys*, and we don’t know what came in between. We also know little about the role of extinction events. ... Yet we have only the wispiest grasp of how and why turtles survived such cataclysmic times.”<sup>12</sup>

Black neglected to mention the major internal organ and structural changes required to evolve a terrestrial animal into a largely aquatic animal like a turtle.

### ***Pappochelys*: the newest claimed example of an intermediate turtle**

Currently, the fossil record does not provide evidence of turtle shell evolution. However, several new examples of potential pre-turtles, claimed by evolutionists, will now be evaluated. Gilbert and his associates have proposed a theoretical embryological model involving movement of the ribs into the dermal layer that is believed to have led, millions of years later, to the evolution of the turtle shell.<sup>15</sup> This modelling, although useful, cannot replace the requirement for paleontological evidence.<sup>16</sup> More fossils and more research has only resulted in biologists telling “dueling stories of how turtles got their shells”.<sup>17</sup>

After admitting that “For years, the oldest turtle fossils we could find had fully formed shells”, the authors of one new discovery claimed that “more primitive fossils are revealing the strange tale of how turtle shells evolved”.<sup>18</sup> What they found, a reptile called *Pappochelys* (meaning grandfather turtle), is nothing like a turtle (figure 2). The claim is based on a large number of small bone fragments meticulously assembled by the paleontologists. From these fragments, the researchers concluded that the *Pappochelys* fossil could fit in the palm of a human hand and grow up to eight inches long. It had a tail comprising about half of its length and used its tiny, peg-like teeth to feed on small insects and worms.

This very non-turtle was speculated to be “a key missing link in the evolutionary history of turtles”.<sup>19</sup> It had neither a carapace nor plastron, but rather the evolutionists speculated that the plastron may have formed by evolution through serial fusion of the gastralia, bones protecting the ventral area of vertebrates.<sup>20</sup> The authors admit “it is difficult to provide a definitive vertebral count for *Pappochelys* based on disarticulated and sometimes disassociated material”.<sup>21</sup> Furthermore, the reconstruction illustrations of the *gastralia* and the *plastron* effectively show the major differences between the two.<sup>22</sup> Schoch and Sues also speculate that “the



**Figure 2.** *Pappochelys*, a supposed turtle ancestor, was clearly a lizard with no evidence of either a carapace or plastron.

Image: Rainer Schoch/CC BY-SA 4.0

Image: Rainer Schoch/CC-BY-SA 4.0



**Figure 3.** Reconstructed skeleton of *Pappochelys* featuring ribs (in orange) and openings in its skull, from which it is argued that turtles did not evolve from early stem reptiles as once thought, but among present-day reptiles that are closely related to lizards. In June 2015, an international team discovered this new extinct reptile, claimed to be a key missing link in the evolution of turtles.

plastron may have first developed as protection and ‘bone ballast’ for controlling buoyancy” in a water environment.<sup>23</sup> *Pappochelys* had a few unique traits; it

“... resembles *Odontochelys* in various features of the limb girdles. Unlike *Odontochelys*, it has a cuirass of robust paired gastralia in place of a plastron. ... Its skull has small upper and ventrally open lower temporal fenestrae, supporting the hypothesis of diapsid affinities of turtles.”<sup>27</sup>

All of the many very different kinds of turtles have one thing in common, which *Pappochelys* also possesses, namely

“... modifications required to live inside this box of bone. Their upper ribs are fused to the inside of their shell and their shoulder joints are set inside their ribs. This anatomical form is unprecedented among vertebrates. Imagine how your arms would move—or rather wouldn’t—if your shoulders were inside your ribcage. ‘It is the shell and associated features, such as the position of the limb girdles inside it, that makes turtles so unusual ... [see figure 3].’”<sup>24</sup>

Furthermore, *Pappochelys* lacked openings located behind the eye socket on each side of the skull which exists both in lizards and crocodilians:

“Look at the back of almost any other reptile skull—whether it is a gecko or a *Tyrannosaurus rex*—and you will see a pair of openings for jaw muscle attachments. Turtle skulls, with their toothless beaks, don’t have these holes, making them an oddity that lacks a clear connection to any other group of reptiles.”<sup>25</sup>

The fact is, “The early evolution of turtles continues to be a contentious issue in vertebrate paleontology.”<sup>26</sup> Thus, “scientists who study the evolution of these animals have a running joke: turtles might as well have come from space.”<sup>27</sup>

### Changes required to evolve a turtle from another reptile

Major changes would be required for a non-turtle reptile to evolve into a turtle, with its unique shell and other features. As will be explained, none of the claims made for ‘transitional forms’ even begin to bridge this gap. The origin of the turtle shell, which “contains over 50 dermal bones found in no other vertebrate order”,<sup>28</sup> is still a major

problem for evolution.<sup>29</sup> The most radical (but not the only) change required to evolve a turtle from a non-turtle is the evolution of the shell. The shell is a box-like structure firmly fused with the turtle’s backbone and ribs. The top shell, the *carapace*, and the lower shell, the *plastron*, are connected by a lateral bridge-like wall on both sides.

These bony shell plates are covered with keratin, the tough substance found

in claws, hair, fingernails, and horns, which protects the shell and reduces water loss.<sup>30</sup> The shell design suggests “daring architectural design with innovative engineering.”<sup>31</sup> Although the main function of the turtle shell is protection, it also serves as a reservoir for water, fat, and wastes and also functions as an effective pH buffer.<sup>31</sup>

Another required change concerns the scapulae (‘shoulder blades’), which in other vertebrates are located *outside* of the rib cage, except in turtles, where they are located *inside* the rib cage (along with the humerus and several other bones).<sup>32</sup> The primitive-reptile turtles are theorized to have evolved from a reptile with three to five cervical vertebrae and, in contrast, turtles have eight. The turtle skull is also very different from that of other reptiles.<sup>33</sup> Turtle skeletal structure is so very different from all other tetrapods that “turtle origins are difficult to resolve without evidence [of these changes] in the fossil record.”<sup>34</sup>

Depending on the turtle type, the dermal layer of the shell generally has a total of 60 bones. The carapace is composed of about 38 paired and 12 unpaired bones, and the plastron has eight paired bones and one unpaired bone. The shell’s epidermal layer is made up of 38 keratinized sections, called scutes, in the carapace and 16 in the plastron.<sup>35</sup> The evolution of the turtle would thus also require the formation of several score new structures besides the shell, including much of the turtle’s bony skeleton.<sup>36</sup> The tetrapod body plan requires not only extensive modification to evolve into a turtle, but also dramatic physiological changes. For example, because the turtle chest is not distensible, the turtle respiratory system is designed very differently from that of all other reptiles.<sup>37</sup>

For these reasons, the “turtle shell represents a classic evolutionary problem: the appearance of a major structural adaptation.”<sup>38</sup>

One hypothesis developed to solve the evolution of turtles problem is the theory that the turtle carapace gradually evolved from “elements of the primitive reptilian integument”.<sup>39</sup> Systematist and reptile expert Olivier Rieppel stated that a big “problem for an evolutionary biologist is to explain these transformations in the context of a gradualistic process.”<sup>40</sup> Rieppel concludes that turtles could not have evolved by any gradual process, so they must be an example of ‘hopeful monsters’, a result of major mutations that cause very rapid evolution called punctuated equilibrium.<sup>41</sup> In short:

“The origin and early evolution of turtles have long

been major contentious issues in vertebrate zoology. This is due to conflicting character evidence from molecules and morphology and a lack of transitional fossils from the critical time interval.”<sup>42</sup>

All of these and hundreds more changes are required for a turtle to evolve from a non-turtle. *Proganochelys* was, and still is, the most primitive known turtle which “was unquestionably a turtle, from its spiky shell to the arrangement of its shoulders and lack of holes in the rear of its skull.”<sup>25</sup> This turtle obviously “wasn’t much help to those trying to figure out how turtles evolved.”<sup>19</sup>

## Conclusions

A huge chasm exists between turtles and their proposed reptilian ancestors. The latest claims of evolutionary links totally fail to bridge this large gap. The origin of turtles remains one of the most problematic claims of evolution and all efforts to fill the gap have failed.

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# Isaac Newton—friend or foe to biblical creation?

Martin Duboisée de Ricquebourg

Isaac Newton has often been cited as a six-day creationist or enrolled favourably in support of biblical creation. Moreover, his chronological writings do seem to allow for a world not much older than 6,000 years. But his less-than-literal treatment of Genesis 1–11 should make creationists cautious to appropriate Newton to this end. There is also reason to believe that Newton was possibly the first to advance the day-age theory, and inspired some of the earliest naturalistic reinterpretations of Genesis 1–11.

Newton has been called “one of the greatest creative men of genius who ever existed”,<sup>1</sup> the “high priest of science”,<sup>2</sup> and the “last of the magicians”.<sup>3</sup> As early as 1728, one reviewer even said that he was “the greatest man in the world, not only in this age, but in any age, since the world began”.<sup>4</sup> His intellectual impact in the world was such that, “it was not till a century after his death that men freed themselves from his authority sufficiently to do important original work in the subjects of which he had treated.”<sup>5</sup>

With a such a legacy it is only natural for creationists to seek to utilise Newton in support of biblical creation. But what were his actual beliefs and how did he treat Genesis 1–11? This paper will show that Newton’s writings on creation, chronology, and the Christian faith were sometimes enigmatic and less than orthodox.

## Newton’s *Principia Mathematica* and *Opticks*

Most of Newton’s seminal work was completed “between the ages of 21 and 23”.<sup>6</sup> In these two years, he “formulated his basic laws of mechanics, his optical observations on the nature of light, the calculus, and the law of universal gravitation”.<sup>7</sup> But his greatest literary masterpiece, published several years later in 1687, was *Philosophiæ Naturalis Principia Mathematica* (figure 1).<sup>8</sup> This book has been praised as the “most famous scientific work of all time”.<sup>9</sup> It is therefore both surprising and significant to realise that Newton wrote more on theology than he ever did on science.<sup>10</sup>

So to what extent did Newton allow his theology to influence his science? Storr, following Keynes,<sup>11</sup> believes that Newton “regarded the riddle of the universe in theological terms.”<sup>12</sup> Even if this assessment is justified, Newton apparently disapproved of the only direct reference to God<sup>13</sup> in the first publication of *Principia*: “God placed the planets at different distances from the sun”,<sup>14</sup> because in

all subsequent editions, he changed it to “the planets were to be placed at different distances from the sun”.<sup>15</sup> This alteration was mitigated by the fact that, to all subsequent editions of *Principia*, he also added a short theologically explicit addendum entitled “General Scholium”. In the General Scholium, Newton writes:

“This most beautiful system of the sun, planets, and comets, could only proceed from the counsel and dominion of an intelligent and powerful Being . . . . This Being governs all things, not as the soul of the world, but as Lord over all; and on account of his dominion he is wont to be called *Lord God* [emphasis in original].”<sup>16</sup>

This is followed by two more pages of theological philosophising, after which Newton concludes, “thus much concerning God; to discourse of whom from the appearances of things, *does certainly belong to natural philosophy* [emphasis added]”.<sup>17</sup> So although Newton removed any explicit theologising from *Principia*, these latter remarks appear to support the idea in principle.

His endorsement of intelligent design can also be found in the second edition of *Opticks*, where Newton wrote, “And tho’ every true step made in this philosophy brings us not immediately to the knowledge of the first cause, yet it brings us nearer to it, and on that account is to be highly valued.”<sup>18</sup> In the fourth edition, he took this even further, saying:

“... the main Business of natural philosophy is to argue from phenomena without feigning hypotheses, and to deduce causes from effects, till we come to the very first cause, which certainly is not mechanical; and not only to unfold the mechanism of the world, but chiefly to resolve these and such like questions.”<sup>19</sup>

Newton had no time for atheism which he regards as “so senseless & odious to mankind that it never had many professors.”<sup>20</sup>

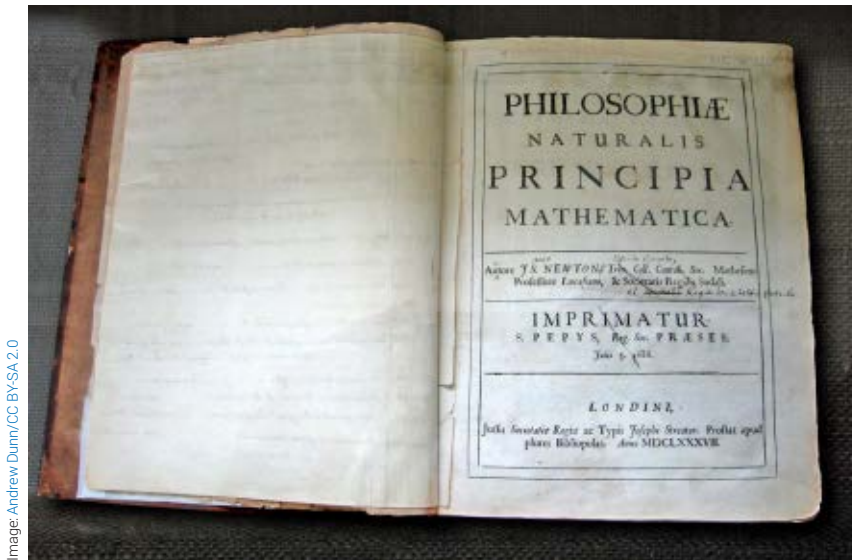


Figure 1. Isaac Newton's own first edition copy of *Philosophiæ Naturalis Principia Mathematica*

### Newton's separation of science and theology

Outside of the Royal Society, Newton was also “unambiguously favourable” toward those who used his system in their own apologetics.<sup>21</sup> For example, in 1692, Newton wrote to Richard Bentley (1662–1742): “When I wrote my treatise about our Systeme I had an eye upon such Principles as might work with considering men for the beleife of a Deity & nothing can rejoyce me more then to find it usefull for that purpose.”<sup>22</sup> But in another short paper, *Seven Statements on Religion*, Newton states as his first principle, “religion & philosophy are to be preserved distinct. We are not to introduce divine revelations into philosophy, nor philosophical opinions into religion.”<sup>23</sup> Moreover, as Manuel relates, “When Newton was President of the [Royal] Society, the journal-books record, he banned anything remotely touching on religion, even apologetics.”<sup>24</sup>

This makes it hard to ascertain, therefore, to what extent Newton allowed theology to infiltrate his science, given that he preferred—if not in principle, at least in practice—to keep the two separate. As Snobelen has observed, there is “more explicit theology in Charles Darwin’s *Origin of Species* (1859) than in the first edition of Newton’s great work.”<sup>25</sup> That said, Snobelen still contends:

“Recent work on early modern science has demonstrated a direct (and positive) relationship between the resurgence of the Hebraic, literal exegesis of the Bible in the Protestant Reformation, and the rise of the empirical method in modern science . . . . In this, Newton also played a pivotal role. As strange as it may sound, science will forever be in the debt of millenarians and biblical literalists [emphasis added].”<sup>26</sup>

This may be true, but Newton does not fit the classification of a traditional ‘biblical literalist’ easily.

### Newton's heterodoxy

Whilst it is not difficult to find evidence of Newton’s enthusiasm for the Bible, his theological views were often heterodox. As Thomas Hearne (1678–1735) once wrote of him:

“Sir Isaac Newton, tho’ a great mathematician, was a man of very little religion, in so much that he is ranked with the heterodox men of the age.”<sup>27</sup>

Likewise, Snobelen concedes that although Newton was a “devoted believer”, in other ways he was a “damnable heretic.”<sup>28</sup> It is hard to dispute the fact that Newton was an Arian.<sup>29</sup> In his treatment on the religion of Newton, Manuel refrains from “pigeonholing” Newton like this, but still concedes that

he was anti-trinitarian.<sup>30</sup> This kind of heterodoxy can be seen in 12 propositions he made on the nature of Christ,<sup>31</sup> and in *Irenicum, or Ecclesiastical Polyty tending to Peace*, where he identifies Jesus as the archangel Michael.<sup>32</sup> Newton also questioned the reality of a literal devil and evil spirits.<sup>33</sup> Yet, Snobelen maintains that “Newton’s demonology was an exegetical option, not a sign of the encroaching Enlightenment.”<sup>34</sup> But this is hard to accept, given that, as Snobelen himself admits:

“Newton’s denial of evil spirits was well outside the theological mainstream in his own day and for a long time afterward. His position would have been viewed as a runaway to infidelity, a capitulation to cold, dark atheism, a disturbing disenchantment of the world or even a delusion inspired by Beelzebub himself. If only his witching-hunting colleagues at the Royal Society had known.”<sup>34</sup>

### Newton's radical friends

Newton’s secrecy in these matters is telling. Moreover, as King and Popkin have argued, Newton’s views were not untouched by the writings of seminal Enlightenment thinkers like Baruch Spinoza (1632–1677) and Richard Simon (1638–1712).<sup>35</sup> As his interpretation of Genesis 36:31 shows, Newton employed the same exegetical argument used by Simon to dismiss the Mosaic authorship of certain sections of Genesis.<sup>36</sup> He was also good friends of John Locke (1632–1704), widely regarded as “England’s foremost Enlightenment thinker” and “father of liberalism.”<sup>37</sup> Newton asked Locke “in the strictest confidence” to help him translate a controversial treatise on 1 John 5:7 and 1 Timothy 3:6 into

French and have it published anonymously in the Netherlands.<sup>38</sup> The treatise was entitled *An historical account of two notable corruptions of Scripture* and was addressed to Jean Le Clerc (1657–1736),<sup>39</sup> “Europe’s most tenacious protagonist of rationalist Christian theology”.<sup>40</sup> Thus Popkin writes:

“Newton, like Spinoza and Simon, took seriously the problems that had arisen in the collection, editing, and transmission of Scripture that made it difficult if not impossible to find the pure original text. Newton, unlike the fundamentalists of the past century and a half, *was not committed to claiming the inerrancy of the biblical text*, but was committed to finding its message for mankind [emphasis added]”.<sup>41</sup>

Whilst Popkin may be overstating the case, the fact remains that Newton was not untouched by the kind of thinking that fuelled the Enlightenment. Put more strongly, Newton’s contribution to the sciences and theology did little to hinder its development. As Israel observes:

“Although down to 1750, in Europe as a whole, the struggle for the middle ground remained inconclusive, much of the European mainstream had, by the 1730s and 1740s, firmly espoused the ideas of Locke and Newton which indeed seemed uniquely attuned and suited to the moderate Enlightenment purpose.”<sup>42</sup>

So although Newton “devoted close to six decades to a passionate study of the Bible, theology, prophecy, church history and natural theology”, his heterodox reading of Scripture left room for a less-than-literal interpretation of Genesis.<sup>43</sup>

### Newton’s earlier treatment of Genesis

In 1680, Thomas Burnet (1635–1715) sent Newton a pre-publication copy of *Telluris theoria sacra* (1681) for review. Burnet wanted to establish scientific reasons to “justify the doctrines of the *Universal Deluge*, and of a *Paradisiacal State*, and protect them from the cavils of those that are no well-wishers to sacred history”.<sup>44</sup> In the correspondence which ensued, Newton suggests that the “heat of the sun” might explain how the oceans were formed and dry land appeared on the earth.<sup>45</sup> This imaginative re-interpretation of Genesis 1:9 requires the “diurnal revolutions of the Earth” to be “very slow” at the beginning of creation so that “the first 6 revolutions or days might continue time enough for the whole Creation, & ye Sun in that time might convert & shrink the parts of the Earth about the Æquator”.<sup>45</sup> In his reply to Newton, Burnet points out that the sun was only made later in the week:

“... methinks you forget Moses (whom in another place you will not suffer us to recede from) in this account of the formation of the Earth; for hee makes

the seas & dry land to bee diuided & the Earth wholly formed before the Sun or Moon existed. These were made the fourth day according to Moses, & the Earth was finished the 3<sup>d</sup> day.”<sup>46</sup>

This gives Newton cause to explain, in the letter which follows, that Genesis 1–2 was written phenomenologically to describe what Moses would have seen, had he been there to witness it himself.<sup>46</sup> The point is not to read Genesis as science or as fiction, says Newton.<sup>47</sup> Instead, Genesis is a “true description” of creation accommodated to the “vulgar” understanding of Moses’ first readers.<sup>48</sup> Taken on its own, Newton’s overall conclusion is both conservative and orthodox:

“... me thinks one of the tenn commandments given by God in mount Sina, prest by diuers of the prophets, observed by our Saviour, his Apostles & first Christians for 300 years & with a day’s alteration by all Christians to this day, should not be grounded on a fiction.”<sup>49</sup>

But this stance does not preclude him from asserting that sun, moon, and stars were not created on “the fourth day nor in any one day of the creation”; that Moses might not mention their creation at all; that the duration of the first and second days might be “as long as you please”; or that Burnet’s theory could allow “a year for each days work” without misinterpreting the text.<sup>47</sup>

### Newton’s later treatment of Genesis

On the whole, it is possible that Newton, at this stage in his career, maintained a more literal approach to Genesis, albeit tenuously. From the mid-to-late 1680s, however, his opinions on Genesis moved in a more radical direction. In a treatise on Revelation,<sup>50</sup> Newton calls the story of the fall of man a “parable”; the trees in Eden, “mystical”; and the serpent, “only a symbol of the spirit of delusion”.<sup>51</sup> With regards to the six days of creation he writes:

“And so the six days of the Creation may signify not only six years but even six thousand years ... or any other six long times. For the history of the creation is not in all things literal. In that Paradise the flaming sword & trees of life & knowledge may be as much figurative descriptions of something we now understand not as the tree of life is in the Paradise to come, & in a parabolical description of the creation a day may be used figuratively as well as other things are especially since there was no light till the end of the first day nor sun till the fourth—to make natural days. The evenings & mornings of Moses respect all parts of the Earth alike so that it was evening all over the Earth in the beginning of each day of Moses & morning all over it in the end of each day: & therefore his evenings & mornings were not natural ones.



ffor had they been natural ones it would have been morning in one part of the Earth when it was evening in another.”<sup>52</sup>

For this reason, it is evident that Newton did not advocate a literal six-day creation,<sup>53</sup> nor was he “committed to the literal truth of Holy Scripture”.<sup>54</sup> Whether or not it was Burnet’s writings that finally convinced him to abandon the literal historicity of the hexameron is not easy to ascertain. What is known, however, is that in Burnet’s subsequent cosmological treatise, *Archaeologiae philosophicae sive doctrina antiqua de rerum originibus* (1692), he calls the story of Adam and Eve a parable; rejects the creation of Eve from Adam’s rib; considers a speaking serpent to be utterly nonsensical; does not believe that Adam and Eve were capable of sewing their own clothes; denies that the Garden of Eden was guarded by real Cherubim; disbelieves that Adam had named all the animals in a single day or that the universe is less than 6,000 years old.<sup>55</sup>

### Newton’s chronology

That said, Newton’s chronological writings do treat aspects of Genesis 1–11 as literal history. He affirms the repopulation of the world from Noah’s sons and traces the origin of nations back to Babel.<sup>56</sup> He also asserts, in the conclusion to the first draft of his chronology of ancient kingdoms, that “mankind could not be older then [*sic*] is represented in scripture”<sup>57</sup> which he later revised to “mankind could not be *much* older than is represented in Scripture [emphasis added]”.<sup>58</sup> Therefore, it is probable that Newton still believed in an earth not much older than 6,000 years. Some scholars even assert that Newton’s chronology depended upon or defended James Ussher’s *Annales veteris testamenti, a prima mundi origine deducti* (1650).<sup>59</sup> But this claim is questionable for the following reasons: firstly, Newton’s chronology does not begin with Adam, it begins with Noah;<sup>60</sup> secondly, the manner in which he places Scripture alongside many other historical sources suggests, as Westfall rightly points out, that “Newton’s view of human history did not centre on the Bible”, but that he “treated the historical books of the Old Testament as human documents to be used in concert with other human documents;”<sup>61</sup> thirdly, Arthur Bedford (1668–1745), a contemporary of Isaac Newton, wrote one of the earliest critiques of *The Chronology of Ancient Kingdoms Amended* (1728) in which he demonstrates how Newton’s chronology “differs *toto caelo* from all the learned men in the world” including, most notably, James Ussher.<sup>62</sup> In fact, I have also not found a single reference, positive or negative, to Ussher within the Newtonian corpus. Finally, in all his chronological writings, Newton never provides an age for

the earth or a date for creation. The omission of such an obvious chronological detail is telling.

Newton (2006:191, 376), nevertheless, is helpfully critical of the Egyptian, Persian, and Syrian records, which “out of vanity” have exaggerated the antiquity of their kingdoms by “some thousands of years older than the world”.<sup>63</sup> Consequently, his stated objective is to correct these erroneous chronologies by referring to the more reliable records preserved by the Greeks and Hebrews.<sup>63,64</sup> But, like Bedford observes: “As to what [Newton] saith, that he hath made it agreeable with sacred history; it is hard to know, whether he was in earnest or in jest.”<sup>65</sup> This is because, in Bedford’s assessment, Newton’s chronology ignores, misquotes, and contradicts the biblical record in several places.<sup>66</sup> His conclusion is forceful: “such poison ought not to go abroad into the world” for it undermines the integrity of the sacred text.<sup>67</sup> For these reasons, we should be hesitant to endorse Newton’s chronology uncritically.

### Newton’s hermeneutical legacy

Burnet was the first to attempt an explanation of Genesis 1–11 in collaboration with Newton himself and in terms of Newtonian physics. And what was the result? A cosmology that had very little to do with Genesis at all. In Burnet’s estimation, “the very letter of the *Hexameron* [is] most absolutely contradictory to the nature of things, as well as to all philosophical reasons” and, “people could neither understand nor bear a plain and philosophical explication of it”.<sup>68</sup> What this called for, in practice, was a *scientific* hermeneutic, whereby “philosophy is the interpreter of Scripture in natural things”.<sup>69</sup> It was a principle that resonated strongly with Charles Blount (1654–1693), the “chief deist of his age”, who eagerly plagiarised sections of Burnet’s writings to further his radical agenda in England.<sup>70</sup>

Like Burnet, William Whiston (1667–1752) wrote his own philosophical version of Genesis 1–11, *A new theory of the Earth* (1696), which he dedicated to Newton. In it he calls literal six-day creation a “vulgar hypothesis”, arguing instead that the days in Genesis should be understood as years.<sup>71</sup> He also argues that Genesis 1 does not tell us how matter came into being or how the universe was created, being restricted exclusively to the origin of the earth.<sup>72</sup> Far from disapproving of Whiston’s theory of the earth, in 1702, Newton appointed him as his successor to the Lucasian chair of mathematics at Cambridge.<sup>73</sup>

Edmund Halley (1656–1742), a close friend and admirer of Newton, also refused to accept that the days in Genesis should be taken as “natural days”.<sup>74</sup> He maintained that the Scriptures could not provide a reliable account of the age of the earth. Instead, Halley proposed that the salinity of the oceans could give a better estimate.<sup>75</sup>



**Figure 2.** A portrait of Isaac Newton by Sir Godfrey Kneller (1689)

In France, Bernard Le Bovier de Fontenelle (1657–1757), the first to publish a biography of Newton,<sup>76</sup> also rejected Genesis 1–11 as literal history. He used his editorial influence at the French *Académie des sciences* to actively promote geological views that precluded the biblical Flood, whilst at the same time censoring any scientific interpretations that assumed or asserted it.<sup>77</sup> Likewise, Voltaire (1694–1778) cites Newton in support of his claim that Genesis was not written by Moses, and calls the Pentateuch a “stupid falsehood” and “absurd fable”, “written by fools, commented upon by simpletons, taught by knaves”, and filled with “innumerable geographical and chronological errors and contradictions”.<sup>78</sup> Comte de Buffon (1708–1788) also employed Newtonian physics in his rigorously naturalistic reinterpretation of Genesis 1–11.<sup>79</sup> This is noteworthy for the simple fact that Buffon, “more than anyone else, was responsible for a new chronology of the earth, that is, for the acceptance of a vast time scale.”<sup>80</sup>

In Germany, one of the most influential philosophers of the last three centuries,<sup>81</sup> Immanuel Kant (1724–1804),

launched his academic career with a scientific treatise entitled, *General natural history and theory of the heavens, or an essay on the constitution and mechanical origin of the whole universe, treated in accordance with Newtonian principles* (1755). In this controversial book, he constrains God to a first cause whilst trying to explain, on Newtonian grounds, how matter could arrange itself into the present universe over time.<sup>82</sup>

Newton might never have anticipated or desired such a legacy, but his influence directly and indirectly affected how Genesis 1–11 would be read by future generations.

## Conclusion

For the 1680s, Newton’s treatment of Genesis was far from orthodox, and possibly the first articulation of the day-age hypothesis in history. If correct, this makes Newton a key figure in the ensuing hermeneutical revolution which shaped how Genesis 1–11 would be read for the next three centuries. This accords well with Israel’s analysis for the onset of the Enlightenment, which he places within the same time period (i.e. from 1650–1680).<sup>83</sup> Thus

the timing of Newton’s comments on Genesis, dated to the late 1680s, happen to correlate strongly with the inauguration of the Enlightenment period.<sup>84</sup> Prophetically perhaps, in the front matter of the first edition of *Principia*, Halley regards Newton as superior to Moses, “Who opens the treasure chest of hidden truth . . . No closer to the gods can any mortal rise.”<sup>85</sup> The curious corollary to all this, is that Newton accepted such praise in print as the foreword to his *magnum opus*. Did Newton think of himself as Moses’ scientific successor? Perhaps, perhaps not. Either way, Moses did not fare well in the next century. As Manuel has observed, for the Enlightenment to flourish in the 18<sup>th</sup> century, “certain basic intellectual needs” had to be met, the first being: “a replacement of Genesis.”<sup>86</sup> Newton did little to hinder such a venture. It is probable that several theologians from the next generation took their lead from him.<sup>87</sup>

For reasons such as these, Newton’s legacy is a greater hindrance than help to biblical creationists. Although his science was inspired by Scripture, his view of Scripture was increasingly shaped by his science.

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**Martin Riquebourg** graduated from the University of Cape Town with a degree in Computer and Electrical Engineering (B.Sc.). He then spent the next 8 years studying at the Bible Institute of South Africa where he eventually earned a Masters in Theology. During that time he spent two years theologically and philosophically evaluating the life and legacy of Charles Darwin. He went on to serve as the Academic Dean of Harare Theological College from 2012 till 2020. Martin is currently working part-time as a Pastoral Assistant at a Presbyterian Church in Perth. He is also enrolled in a Ph.D. through North-West University (South Africa) to explore how various popular interpretations of Genesis 1–11 have originated.

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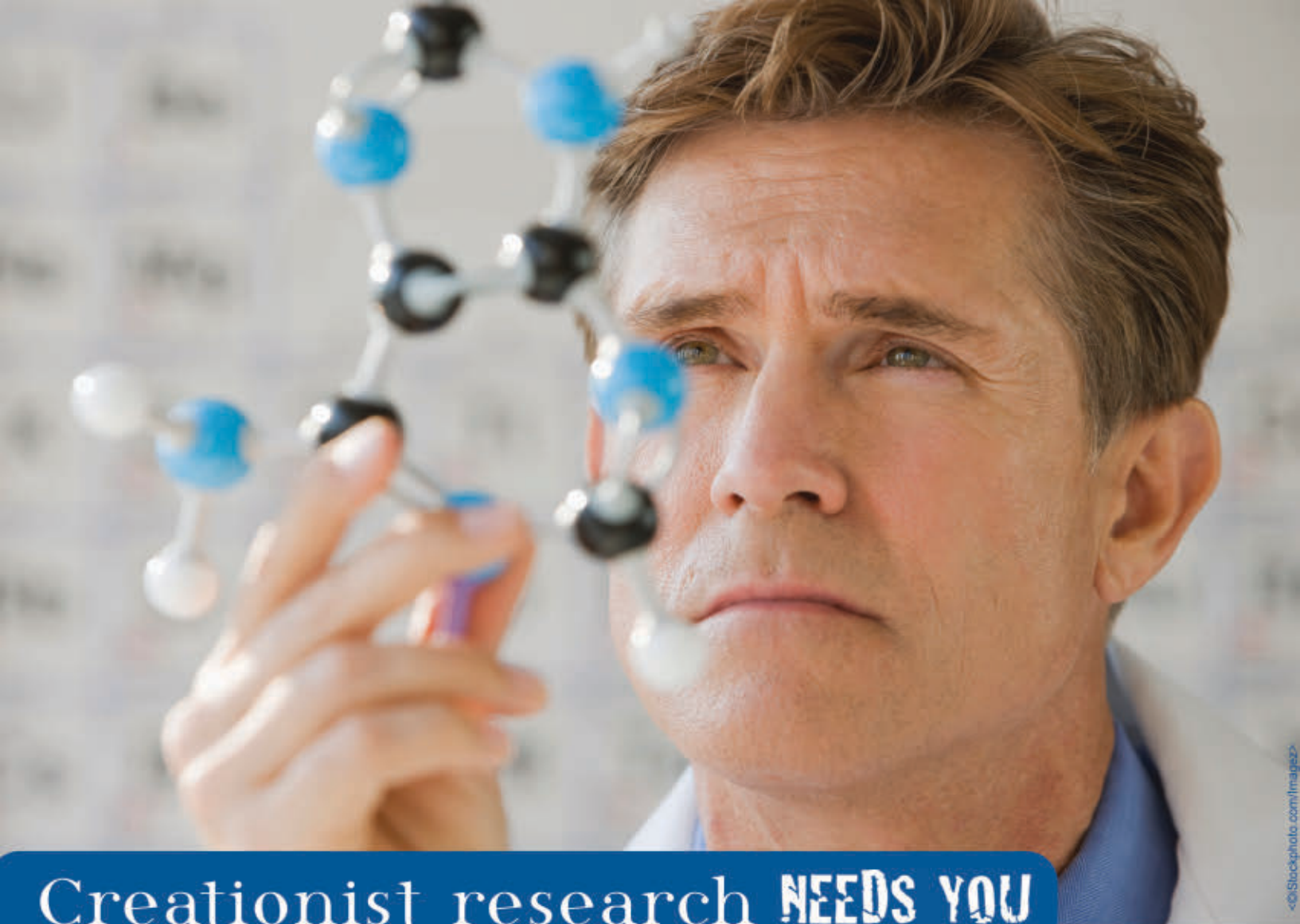
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